

GenCore version 5.1.6  
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OM protein. - protein search, using sw model

Run on: March 11, 2005, 07:17:30 ; Search time 72.9307 Seconds

(without alignments)  
4925.234 Million cell updates/sec

Title: US-10-027-400-2

Perfect score: 5652

Sequence: 1 MGTSHPAFLVGLGLTGLSL.....IDMDDIGIDSDLVDSPL 1089

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5652	100.0	1089	9	US-09-769-987-2
2	5652	100.0	1089	9	US-09-919-497-90
3	5652	100.0	1089	9	US-09-866-510-2
4	5652	100.0	1089	14	US-10-027-400-2
5	5652	100.0	1089	15	US-10-394-322A-50
6	5652	100.0	1089	15	US-10-367-639-35
7	5652	100.0	1089	16	US-10-322-696-168
8	5652	100.0	1089	16	US-10-741-601-439
9	5652	100.0	1089	17	US-10-741-600-1304
10	5649	99.9	1089	9	US-09-866-510-10
11	5648	99.9	1089	9	US-09-866-510-4
12	5648	99.9	1089	9	US-09-955-363-36
13	5647	99.9	1089	9	US-09-866-510-8

14	5646	99.9	1089	9	US-09-866-510-6
15	5636.5	99.7	1088	10	US-09-961-403-4
16	5232	92.6	1096	16	US-10-322-696-165
17	3046	53.9	589	9	US-09-866-510-12
18	2693.5	47.7	834	15	US-10-637-356-2
19	2692	47.6	849	15	US-10-637-356-1
20	2676.5	47.4	811	15	US-10-637-356-4
21	2676.5	47.4	826	15	US-10-637-356-3
22	2425	42.9	460	16	US-10-664-421-64
23	2354.5	41.7	1106	9	US-09-866-510-22
24	2354.5	41.7	1106	9	US-09-955-363-2
25	2354.5	41.7	1106	15	US-10-394-322A-51
26	2354.5	41.7	1106	15	US-10-367-639-36
27	2351.5	41.6	1106	14	US-10-027-400-4
28	2350.5	41.6	1106	9	US-09-866-510-16
29	2349.5	41.6	1106	9	US-09-866-510-20
30	2348.5	41.6	1106	9	US-09-866-510-18
31	2347	41.5	1090	9	US-09-866-510-14
32	2031	35.9	386	9	US-09-939-754-6
33	2031	35.9	386	9	US-09-939-832-6
34	2031	35.9	386	9	US-09-939-833-6
35	1499.5	26.5	293	16	US-10-763-418-16
36	1454.5	25.7	976	13	US-10-099-895-32
37	1454.5	25.7	976	14	US-10-192-867-4
38	1454.5	25.7	976	15	US-10-295-027-708
39	1454.5	25.7	976	15	US-10-457-954-2
40	1446.5	25.6	975	14	US-10-192-867-2
41	1346.5	23.8	972	9	US-09-944-807-10
42	1346.5	23.8	972	17	US-10-741-600-1570
43	1346.5	23.8	972	17	US-10-741-600-1571
44	1340.5	22.7	806	16	US-10-408-765A-2335
45	1287	22.8	1338	14	US-10-060-065-23

#### ALIGNMENTS

RESULT 1

US-09-769-987-2  
; Sequence 2, Application US/09769987  
; Patent No. US20020055129A1  
; GENERAL INFORMATION:  
; APPLICANT: Matsui, Toshimitsu  
; APPLICANT: Aaronson, Stuart A.  
; APPLICANT: Pierce, Jacalyn H.  
; TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor  
; FILE REFERENCE: 14014.026602  
; CURRENT APPLICATION NUMBER: US/09/769,987  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 08/460,656  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: US 08/439,095  
; PRIOR FILING DATE: 1995-05-11  
; PRIOR APPLICATION NUMBER: US 07/915,884  
; PRIOR FILING DATE: 1992-07-20  
; PRIOR APPLICATION NUMBER: US 07/308,282  
; PRIOR FILING DATE: 1989-02-09  
; NUMBER OF SEQ IDS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1089  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; No. US20020055129A1 =  
; OTHER INFORMATION: synthetic construct  
US-09-769-987-2

Query Match 100.0%; Score 5652; DB 9; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 1.2e-311;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVGLGLTGLSLPILPNEKVVQLNSFSLRCFGESEVSWQYP 60

Db	1	MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSRLCFGESEVSWQYP	60
Qy	61	MSEEESSDVEIRNEENNSGLFVTVLVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY	120
Db	61	MSEEESSDVEIRNEENNSGLFVTVLVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY	120
Qy	121	VPDPDAFVPLGMDVLYIVVEDDDSAIIPCRITDPTPTVTLHNSGVVPASYSRQGFNG	180
Db	121	VPDPDAFVPLGMDVLYIVVEDDDSAIIPCRITDPTPTVTLHNSGVVPASYSRQGFNG	180
Qy	181	TFTVGPVYCEATVKGKGFQTIIPFNVALKATSELDLEMEALKTIVYKSGETIVVTCVAFNN	240
Db	181	TFTVGPVYCEATVKGKGFQTIIPFNVALKATSELDLEMEALKTIVYKSGETIVVTCVAFNN	240
Qy	241	EVVDLQWTPYGEVKGKGIITMLEIKVPSIKLVYTLVTPVPEATVKDSDGYECAARQATREVK	300
Db	241	EVVDLQWTPYGEVKGKGIITMLEIKVPSIKLVYTLVTPVPEATVKDSDGYECAARQATREVK	300
Qy	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVHFVVEVRAVPPPRISWLNKNTLIENL	360
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVHFVVEVRAVPPPRISWLNKNTLIENL	360
Qy	361	TEITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSIIDL	420
Db	361	TEITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSIIDL	420
Qy	421	VDDHSGTGQTVRCCTAEGTPLDIEWMICKDIKKCNNETSWILANNVSNIIITEHSRD	480
Db	421	VDDHSGTGQTVRCCTAEGTPLDIEWMICKDIKKCNNETSWILANNVSNIIITEHSRD	480
Qy	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKVAPTLRSELIVAAVLVLLVIVII	540
Db	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKVAPTLRSELIVAAVLVLLVIVII	540
Qy	541	SLIVLVVIMKQPRYBIRWRVIESIPDQHEVIYVDPMLPYDPSRWEFFPDGLVLRVLG	600
Db	541	SLIVLVVIMKQPRYBIRWRVIESIPDQHEVIYVDPMLPYDPSRWEFFPDGLVLRVLG	600
Qy	601	SGAFKGVVEGTAYGLRSQFVMKVAVKMLKPTARSEKQALMSELKIMTHLPHLNVNL	660
Db	601	SGAFKGVVEGTAYGLRSQFVMKVAVKMLKPTARSEKQALMSELKIMTHLPHLNVNL	660
Qy	661	LGACTKSGPIYIITEYCFYGDVLYLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY	720
Db	661	LGACTKSGPIYIITEYCFYGDVLYLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY	720
Qy	721	VILSFENNGDYMCKQADTTQYVPMLEKEVSKYSIQRSLYDRPASYYKKSMLDSEVKN	780
Db	721	VILSFENNGDYMCKQADTTQYVPMLEKEVSKYSIQRSLYDRPASYYKKSMLDSEVKN	780
Qy	781	LISDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LISDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Qy	841	RDIMHDSNVYKSGSTFLPVKMAPESEIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMW	900
Db	841	RDIMHDSNVYKSGSTFLPVKMAPESEIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMW	900
Qy	901	VDSTFYNKIKSGYRMKAPDHATSEVTEIMVKCNWSEPEKPSYHLSIEIVENLLPGQYKK	960
Db	901	VDSTFYNKIKSGYRMKAPDHATSEVTEIMVKCNWSEPEKPSYHLSIEIVENLLPGQYKK	960
Qy	961	SYEKIHLDFLKSHPHAPVARMRVSDNAYIGVTYKNEEDKLKOWEGGLDEORLSADSGYII	1020
Db	961	SYEKIHLDFLKSHPHAPVARMRVSDNAYIGVTYKNEEDKLKOWEGGLDEORLSADSGYII	1020
Qy	1021	PLPDIDPVPEEDLGKRNHSSQTSESALETGSSSSTFIKREDETIEDIMDDIGIDS	1080
Db	1021	PLPDIDPVPEEDLGKRNHSSQTSESALETGSSSSTFIKREDETIEDIMDDIGIDS	1080
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Db	1081	SDLVEDSFL 1089	
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; Sequence 90, Application US/09919497			
; Patent No. US2002010662A1			
; GENERAL INFORMATION:			
; APPLICANT: Mutter, George L.			
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER			
; FILE REFERENCE: B0801/7225			
; CURRENT APPLICATION NUMBER: US/09/919,497			
; CURRENT FILING DATE: 2001-07-31			
; PRIOR APPLICATION NUMBER: US 60/221,735			
; PRIOR FILING DATE: 2000-07-31			
; NUMBER OF SEQ ID NOS: 100			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 90			
; LENGTH: 1089			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-919-497-90			
Query Match 100.0%; Score 5652; DB 9; Length 1089;			
Best Local Similarity 100.0%; Pred. No. 1.2e-311;			
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSRLCFGESEVSWQYP	60
Qy	61	MSEEESSDVEIRNEENNSGLFVTVLVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY	120
Db	61	MSEEESSDVEIRNEENNSGLFVTVLVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY	120
Qy	121	VPDPDAFVPLGMDVLYIVVEDDDSAIIPCRITDPTPTVTLHNSGVVPASYSRQGFNG	180
Db	121	VPDPDAFVPLGMDVLYIVVEDDDSAIIPCRITDPTPTVTLHNSGVVPASYSRQGFNG	180
Qy	181	TFTVGPVYCEATVKGKGFQTIIPFNVALKATSELDLEMEALKTIVYKSGETIVVTCVAFNN	240
Db	181	TFTVGPVYCEATVKGKGFQTIIPFNVALKATSELDLEMEALKTIVYKSGETIVVTCVAFNN	240
Qy	241	EVVDLQWTPYGEVKGKGIITMLEIKVPSIKLVYTLVTPVPEATVKDSDGYECAARQATREVK	300
Db	241	EVVDLQWTPYGEVKGKGIITMLEIKVPSIKLVYTLVTPVPEATVKDSDGYECAARQATREVK	300
Qy	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVHFVVEVRAVPPPRISWLNKNTLIENL	360
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVHFVVEVRAVPPPRISWLNKNTLIENL	360
Qy	361	TEITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSIIDL	420
Db	361	TEITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSIIDL	420
Qy	421	VDDHSGTGQTVRCCTAEGTPLDIEWMICKDIKKCNNETSWILANNVSNIIITEHSRD	480
Db	421	VDDHSGTGQTVRCCTAEGTPLDIEWMICKDIKKCNNETSWILANNVSNIIITEHSRD	480
Qy	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKVAPTLRSELIVAAVLVLLVIVII	540
Db	481	RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKVAPTLRSELIVAAVLVLLVIVII	540
Qy	541	SLIVLVVIMKQPRYBIRWRVIESIPDQHEVIYVDPMLPYDPSRWEFFPDGLVLRVLG	600
Db	541	SLIVLVVIMKQPRYBIRWRVIESIPDQHEVIYVDPMLPYDPSRWEFFPDGLVLRVLG	600
Qy	601	SGAFKGVVEGTAYGLRSQFVMKVAVKMLKPTARSEKQALMSELKIMTHLPHLNVNL	660
Db	601	SGAFKGVVEGTAYGLRSQFVMKVAVKMLKPTARSEKQALMSELKIMTHLPHLNVNL	660
Qy	661	LGACTKSGPIYIITEYCFYGDVLYLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY	720

Db 661 LGACTSGPIIYITEYCFYGDVLYNHLKRDSPFLSHHPKPKKELDI FGLNPADESTRSY 720  
QY 721 VILSFENNGDYMDKQADTTQYVPMLERKEVSKYSDIQSLYDRPAS YKKKSMLDSEVK 780  
Db 721 VILSFENNGDYMDKQADTTQYVPMLERKEVSKYSDIQSLYDRPAS YKKKSMLDSEVK 780  
QY 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
Db 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
QY 841 RDIHDSNYSYKSGSTPLPVKMWAPESIFDNLYTTLSDVMSYGLLWEI FSLGGTPYPGMM 900  
Db 841 RDIHDSNYSYKSGSTPLPVKMWAPESIFDNLYTTLSDVMSYGLLWEI FSLGGTPYPGMM 900  
QY 901 VDSFTFNKIKSGYRMKAPDHATSEVYIIMVKWCNSEPEKPSFYHLSEVENLLPGQYKK 960  
Db 901 VDSFTFNKIKSGYRMKAPDHATSEVYIIMVKWCNSEPEKPSFYHLSEVENLLPGQYKK 960  
QY 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTVYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
Db 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTVYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
QY 1021 PLPDDIPVPEEEDLGRNHRSSQTSSESATETGSSSTFIKREDETIEDIMDDDIGIDS 1080  
Db 1021 PLPDDIPVPEEEDLGRNHRSSQTSSESATETGSSSTFIKREDETIEDIMDDDIGIDS 1080  
QY 1081 SOLVEDSFL 1089  
Db 1081 SOLVEDSFL 1089

RESULT 3  
US-09-866-510-2  
; Sequence 2, Application US/09866510  
; Patent No. US20020113041  
; GENERAL INFORMATION:  
; APPLICANT: KAZLAUSKAS, ANDRIUS  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES  
; FILE REFERENCE: ERM-104.01  
; CURRENT APPLICATION NUMBER: US/09/866,510  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/250,747  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 60/289,103  
; PRIOR FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1089  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-866-510-2

Query Match 100.0%; Score 5652; DB 9; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 1.2e-311;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGTSHPAFLVGLGCLLTGLSLILCOLSLPILPNEKVKVQLNSSFSLRCFGESEVSQWYP 60  
QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120  
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120  
QY 121 VPDPAVAFPLGMDTYLVIVEDDSDAIIPCRTPDPTPTVTLHNSGVPASVDSRQGFNG 180  
Db 121 VPDPAVAFPLGMDTYLVIVEDDSDAIIPCRTPDPTPTVTLHNSGVPASVDSRQGFNG 180  
QY 181 TPTVGPYICVATVKGKFKQTIIPNNVYALKATSELDLMEALKTVYKSGETIVVTCAVFN 240  
Db 181 TPTVGPYICVATVKGKFKQTIIPNNVYALKATSELDLMEALKTVYKSGETIVVTCAVFN 240

QY 241 EVVDLQWTPYGEVKGKGIITMLBEIKVPSIKLVVTLTVPATVKDSGDYECARQATREV 300  
Db 241 EVVDLQWTPYGEVKGKGIITMLBEIKVPSIKLVVTLTVPATVKDSGDYECARQATREV 300  
QY 301 EMKKVTIISVHEKGFBIKPTFSQLEAVNLHEVKHFVVEYRAPPRIISMLKNNLTILN 360  
Db 301 EMKKVTIISVHEKGFBIKPTFSQLEAVNLHEVKHFVVEYRAPPRIISMLKNNLTILN 360  
QY 361 TEITTDVEKIQIRVRSKLKIRAKEEDSGHTYIQAQNEADAVKSYTFELLTQVPSITDL 420  
Db 361 TEITTDVEKIQIRVRSKLKIRAKEEDSGHTYIQAQNEADAVKSYTFELLTQVPSITDL 420  
QY 421 VDDHSGTGGQVRCRTAEGTPLPDIEWMIKDIKKCNNETSWTILANNYSNIITEIHSR 480  
Db 421 VDDHSGTGGQVRCRTAEGTPLPDIEWMIKDIKKCNNETSWTILANNYSNIITEIHSR 480  
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540  
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540  
QY 541 SLIVLVVWIKQPRVIRWRVIESIPDGHEIYVDPMLPYDSRWEFPRDGLVLRVLG 600  
Db 541 SLIVLVVWIKQPRVIRWRVIESIPDGHEIYVDPMLPYDSRWEFPRDGLVLRVLG 600  
QY 601 SGAFKGVVEGTAYGLSRSPQVMKVAVMKLTARSSSEKQALMSELKIMTHLGPLHINVL 660  
Db 601 SGAFKGVVEGTAYGLSRSPQVMKVAVMKLTARSSSEKQALMSELKIMTHLGPLHINVL 660  
QY 661 LGACTKSGPIIYITEYCFYGDVLYNHLKRDSPFLSHHPKPKKELDI FGLNPADESTRSY 720  
Db 661 LGACTKSGPIIYITEYCFYGDVLYNHLKRDSPFLSHHPKPKKELDI FGLNPADESTRSY 720  
QY 721 VILSFENNGDYMDKQADTTQYVPMLERKEVSKYSDIQSLYDRPAS YKKKSMLDSEVK 780  
Db 721 VILSFENNGDYMDKQADTTQYVPMLERKEVSKYSDIQSLYDRPAS YKKKSMLDSEVK 780  
QY 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
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QY 841 RDIHDSNYSYKSGSTPLPVKMWAPESIFDNLYTTLSDVMSYGLLWEI FSLGGTPYPGMM 900  
Db 841 RDIHDSNYSYKSGSTPLPVKMWAPESIFDNLYTTLSDVMSYGLLWEI FSLGGTPYPGMM 900  
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Db 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTVYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
QY 1021 PLPDDIPVPEEEDLGRNHRSSQTSSESATETGSSSTFIKREDETIEDIMDDDIGIDS 1080  
Db 1021 PLPDDIPVPEEEDLGRNHRSSQTSSESATETGSSSTFIKREDETIEDIMDDDIGIDS 1080  
QY 1081 SOLVEDSFL 1089  
Db 1081 SOLVEDSFL 1089

RESULT 4  
US-10-027-400-2  
; Sequence 2, Application US/10027400  
; Publication No. US20030017535A1  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, Lewis T.  
; ESCOBEDO, Jaime A.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market, Steuart Street Tower, 20th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/027.400  
FILING DATE: 19-Dec-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/461.917  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US/07/151.414  
FILING DATE: 02-FEB-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.

REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 2307K-267-2-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/326-2400  
TELEFAX: 415/326-2422

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1089 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-027-400-2

Query Match 100.0%; Score 5652; DB 14; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 1.2e-311;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVGLGTLGLSLILCOLSLPSTLPNEKVKVQLNSFSLRCFGESEVSWQYP 60  
DB 1 MGTSHPAFLVGLGTLGLSLILCOLSLPSTLPNEKVKVQLNSFSLRCFGESEVSWQYP 60  
QY 61 MSEEESDVEIRNEENNSGLFVTLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYIY 120  
DB 61 MSEEESDVEIRNEENNSGLFVTLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYIY 120  
QY 121 VPDPAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLNSEGVPVPAVSDSRQGFNG 180  
DB 121 VPDPAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLNSEGVPVPAVSDSRQGFNG 180  
QY 181 TPTVGPVYCEATVKGKGFOTIPNNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
DB 181 TPTVGPVYCEATVKGKGFOTIPNNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
QY 241 EVVDLQWTPYGEVKGKGTIMLEIKVPSIKLVYTLVTPVATVKDSDGYECAAQATREVK 300  
DB 241 EVVDLQWTPYGEVKGKGTIMLEIKVPSIKLVYTLVTPVATVKDSDGYECAAQATREVK 300  
QY 301 EMKKVTISVHEKGFIEIKPTFSOLEAVNLHVKHVFFVVRAYPPPRISWLNKLNLIENL 360  
DB 301 EMKKVTISVHEKGFIEIKPTFSOLEAVNLHVKHVFFVVRAYPPPRISWLNKLNLIENL 360  
QY 361 TEITTDVEKIQEIRYRSKLIKIRAKEDSGHYTIIVAQNEDAVKSYTFELLTQVPSIIDL 420  
DB 361 TEITTDVEKIQEIRYRSKLIKIRAKEDSGHYTIIVAQNEDAVKSYTFELLTQVPSIIDL 420  
QY 421 VDDHSGTGQVRCVTAEGTLPDIEWMICKDKKCNNETSWTILANNVSNITIEIHSRD 480  
DB 421 VDDHSGTGQVRCVTAEGTLPDIEWMICKDKKCNNETSWTILANNVSNITIEIHSRD 480  
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLSLSELTVAAAVLVIVII 540

DB 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLSLSELTVAAAVLVIVII 540  
QY 541 SLIVLVIIWKQKPRYRIRWRVIESPDGHEVIYVDPQMLPYDSRWEFFRDGLVGRVLG 600  
DB 541 SLIVLVIIWKQKPRYRIRWRVIESPDGHEVIYVDPQMLPYDSRWEFFRDGLVGRVLG 600  
QY 601 SGAFKVGVEGTAYGLSRQPVNKMVKMLKPTARSEKQALMSELKIMTHLPHLNVNL 660  
DB 601 SGAFKVGVEGTAYGLSRQPVNKMVKMLKPTARSEKQALMSELKIMTHLPHLNVNL 660  
QY 661 LGACTKSGPIYIITEYCFYGDLYNVLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
DB 661 LGACTKSGPIYIITEYCFYGDLYNVLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
QY 721 VILSPENNGDYMDKQADTTQVPMLEKEVEKVDIOESLYDRPASVKKKMLSEVKN 780  
DB 721 VILSPENNGDYMDKQADTTQVPMLEKEVEKVDIOESLYDRPASVKKKMLSEVKN 780  
QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNVCVHRDLAARNVLLAOGKI VKICDFGLA 840  
DB 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNVCVHRDLAARNVLLAOGKI VKICDFGLA 840  
QY 841 RDIMHDSNVKSGSTFLPVKNWAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGNM 900  
DB 841 RDIMHDSNVKSGSTFLPVKNWAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGNM 900  
QY 901 VDSFTYKIKSGYRMAKPDHATSEVVEIMVKWCNSEPEKRPSPFYHLSEIVENLLPQYKK 960  
DB 901 VDSFTYKIKSGYRMAKPDHATSEVVEIMVKWCNSEPEKRPSPFYHLSEIVENLLPQYKK 960  
QY 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTVYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
DB 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTVYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
QY 1021 PLPDDIDPVEEEDLGRNHRSSQTSEESAIEFGSSSTFIKREDETIEDIMDDDIGIDS 1080  
DB 1021 PLPDDIDPVEEEDLGRNHRSSQTSEESAIEFGSSSTFIKREDETIEDIMDDDIGIDS 1080  
QY 1081 SDLVEDSFL 1089  
DB 1081 SDLVEDSFL 1089

RESULT 5  
US-10-394-322A-50  
; Sequence 50, Application US/10394322A  
; Publication No. US2003023291A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.  
; APPLICANT: Prescott, John C.  
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS  
; FILE REFERENCE: 39750-0006 US  
; CURRENT APPLICATION NUMBER: US/10/394,322A  
; CURRENT FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,892  
; PRIOR FILING DATE: 2002-03-21  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 50  
; LENGTH: 1089  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-322A-50

Query Match 100.0%; Score 5652; DB 15; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 1.2e-311;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGTSHPAFLVGLGTLGLSLILCOLSLPSTLPNEKVKVQLNSFSLRCFGESEVSWQYP 60  
DB 1 MGTSHPAFLVGLGTLGLSLILCOLSLPSTLPNEKVKVQLNSFSLRCFGESEVSWQYP 60  
QY 61 MSEEESDVEIRNEENNSGLFVTLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYIY 120



```
Db 61 MSEESESSVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENLEGRHIYI 120
Qy 121 VDPDPVAFPLGWTDLVTVLEDDSDAIIPCRITDPTPTVTLHNSGVWPASVDSROGFG 180
Db 121 VDPDPVAFPLGWTDLVTVLEDDSDAIIPCRITDPTPTVTLHNSGVWPASVDSROGFG 180
Qy 181 TPTVGPYICEATVKGKGFQIPFNVALKATSELDLEMEALKTIVYKSGETIVVTCVAFNN 240
Db 181 TPTVGPYICEATVKGKGFQIPFNVALKATSELDLEMEALKTIVYKSGETIVVTCVAFNN 240
Qy 241 EVVDLQWTVPGVKGKGTIMLEBEIKVPSIKLVYTLTVPEATVKDSDYECARQATREV 300
Db 241 EVVDLQWTVPGVKGKGTIMLEBEIKVPSIKLVYTLTVPEATVKDSDYECARQATREV 300
Qy 301 EMKVTIISVHEKGFIEIKPTFSOLEAVNLHEVKHFVVEVRAYPPPRISMLKNLTLE 360
Db 301 EMKVTIISVHEKGFIEIKPTFSOLEAVNLHEVKHFVVEVRAYPPPRISMLKNLTLE 360
Qy 361 TEITTDVEKIQIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420
Db 361 TEITTDVEKIQIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420
Qy 421 VDDHSGTGQVRCCTAEGTPLDIEWMICKOIKKNNETSWTILANNVSNITTEIHSRD 480
Db 421 VDDHSGTGQVRCCTAEGTPLDIEWMICKOIKKNNETSWTILANNVSNITTEIHSRD 480
Qy 481 RSTVEGRVTFPAKVEETIAVRCLAKNLGAENRELKLVAPTLSELTVAAAVLVLLVIV 540
Db 481 RSTVEGRVTFPAKVEETIAVRCLAKNLGAENRELKLVAPTLSELTVAAAVLVLLVIV 540
Qy 541 SLVLVVIWKQPRYRIRWRVIESIPDGHXYIYVDPMLPYDSRWEFFPRDGLVLRVLG 600
Db 541 SLVLVVIWKQPRYRIRWRVIESIPDGHXYIYVDPMLPYDSRWEFFPRDGLVLRVLG 600
Qy 601 SGAFKVVEGTAYGLSRSPQVMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNL 660
Db 601 SGAFKVVEGTAYGLSRSPQVMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNL 660
Qy 661 LGACTKSGPIYIITEYCFYGDVNLVHLKNRDPSLHHPKPKKELDI FGLNPADESTRY 720
Db 661 LGACTKSGPIYIITEYCFYGDVNLVHLKNRDPSLHHPKPKKELDI FGLNPADESTRY 720
Qy 721 VILSPENNGDYMDKQADTTQVVPMLERKEVSKYSDIQRSLYDRPASYYKKSKMLDSEVN 780
Db 721 VILSPENNGDYMDKQADTTQVVPMLERKEVSKYSDIQRSLYDRPASYYKKSKMLDSEVN 780
Qy 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQOKIYKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQOKIYKICDFGLA 840
Qy 841 RDIHDSNVYKSGSTFLPVKNWAPESIPDNLVYTLSDVMSYGILLWEIFSLGTPYPGMM 900
Db 841 RDIHDSNVYKSGSTFLPVKNWAPESIPDNLVYTLSDVMSYGILLWEIFSLGTPYPGMM 900
Qy 901 VDSFTFNKIKSGYRMAKPDHATSEVYEIMVKNWSEPEKRPSPFYHLSEIVENLLPCQYK 960
Db 901 VDSFTFNKIKSGYRMAKPDHATSEVYEIMVKNWSEPEKRPSPFYHLSEIVENLLPCQYK 960
Qy 961 SYEKIHLDFLKSHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDQRLSADSGYII 1020
Qy 1021 PLPDDIPVEEDLGRNHRSSQTSSESAIETGSSSSTFIKREDETIEDIMDDIDIGIDS 1080
Db 1021 PLPDDIPVEEDLGRNHRSSQTSSESAIETGSSSSTFIKREDETIEDIMDDIDIGIDS 1080
Qy 1081 SLDVEDSFL 1089
Db 1081 SLDVEDSFL 1089
```

```
US-10-367-639-35
; Sequence 35, Application US/10367639
; Publication NO. US20040001807A1
; GENERAL INFORMATION:
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Edelberg, Jay M.
; APPLICANT: Rafii, Shahin
; APPLICANT: Hong, Mun K.
; APPLICANT: Lanza, Robert P.
; APPLICANT: West, Michael D.
; TITLE OF INVENTION: Endothelial Precursor Cells for Enhancing and Restoring Vascular
; FILE REFERENCE: 1676.004US1
; CURRENT APPLICATION NUMBER: US/10/367,639
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-639-35
```

```
Query Match 100.0%; Score 5652; DB 15; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSQWYP 60
Db 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSQWYP 60
Qy 61 MSEESESSVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENLEGRHIYI 120
Db 61 MSEESESSVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENLEGRHIYI 120
Qy 121 VDPDPVAFPLGWTDLVTVLEDDSDAIIPCRITDPTPTVTLHNSGVWPASVDSROGFG 180
Db 121 VDPDPVAFPLGWTDLVTVLEDDSDAIIPCRITDPTPTVTLHNSGVWPASVDSROGFG 180
Qy 181 TPTVGPYICEATVKGKGFQIPFNVALKATSELDLEMEALKTIVYKSGETIVVTCVAFNN 240
Db 181 TPTVGPYICEATVKGKGFQIPFNVALKATSELDLEMEALKTIVYKSGETIVVTCVAFNN 240
Qy 241 EVVDLQWTVPGVKGKGTIMLEBEIKVPSIKLVYTLTVPEATVKDSDYECARQATREV 300
Db 241 EVVDLQWTVPGVKGKGTIMLEBEIKVPSIKLVYTLTVPEATVKDSDYECARQATREV 300
Qy 301 EMKVTIISVHEKGFIEIKPTFSOLEAVNLHEVKHFVVEVRAYPPPRISMLKNLTLE 360
Db 301 EMKVTIISVHEKGFIEIKPTFSOLEAVNLHEVKHFVVEVRAYPPPRISMLKNLTLE 360
Qy 361 TEITTDVEKIQIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420
Db 361 TEITTDVEKIQIRYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420
Qy 421 VDDHSGTGQVRCCTAEGTPLDIEWMICKOIKKNNETSWTILANNVSNITTEIHSRD 480
Db 421 VDDHSGTGQVRCCTAEGTPLDIEWMICKOIKKNNETSWTILANNVSNITTEIHSRD 480
Qy 481 RSTVEGRVTFPAKVEETIAVRCLAKNLGAENRELKLVAPTLSELTVAAAVLVLLVIV 540
Db 481 RSTVEGRVTFPAKVEETIAVRCLAKNLGAENRELKLVAPTLSELTVAAAVLVLLVIV 540
Qy 541 SLVLVVIWKQPRYRIRWRVIESIPDGHXYIYVDPMLPYDSRWEFFPRDGLVLRVLG 600
Db 541 SLVLVVIWKQPRYRIRWRVIESIPDGHXYIYVDPMLPYDSRWEFFPRDGLVLRVLG 600
Qy 601 SGAFKVVEGTAYGLSRSPQVMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNL 660
Db 601 SGAFKVVEGTAYGLSRSPQVMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNL 660
Qy 661 LGACTKSGPIYIITEYCFYGDVNLVHLKNRDPSLHHPKPKKELDI FGLNPADESTRY 720
Db 661 LGACTKSGPIYIITEYCFYGDVNLVHLKNRDPSLHHPKPKKELDI FGLNPADESTRY 720
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QY 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSIDTQSLYDRPASYKKKSMMLDSEVKN 780
DB 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSIDTQSLYDRPASYKKKSMMLDSEVKN 780

QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840
DB 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840

QY 841 RDIHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900
DB 841 RDIHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900

QY 901 VDSFTFNKIKSGYRMKPDPHATSEVVEIMVKWNSPEKPSFYHLSEIVENLLPGQYKK 960
DB 901 VDSFTFNKIKSGYRMKPDPHATSEVVEIMVKWNSPEKPSFYHLSEIVENLLPGQYKK 960

QY 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII 1020
DB 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII 1020

QY 1021 PLPDIDPVEEDLGRNHRSSQTSSESAIETGSSSTFIKREDETIEDIMMDDIGIDS 1080
DB 1021 PLPDIDPVEEDLGRNHRSSQTSSESAIETGSSSTFIKREDETIEDIMMDDIGIDS 1080

QY 1081 SDLVEDSFL 1089
DB 1081 SDLVEDSFL 1089

RESULT 7
US-10-322-696-168
; Sequence 168, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-696-168

Query Match 100.0%; Score 5652; DB 16; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.2e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVGLGCLLTGLSLILCOLSLPILPNEKVKVOLNSSFSLRCFGESEVSWQYP 60
DB 1 MGTSHPAFLVGLGCLLTGLSLILCOLSLPILPNEKVKVOLNSSFSLRCFGESEVSWQYP 60

QY 61 MSEESESDVEIRNEENNSGLFVTVLVSSAAHTGLTYCYNNHTQTEENLEGRHIYIY 120
DB 61 MSEESESDVEIRNEENNSGLFVTVLVSSAAHTGLTYCYNNHTQTEENLEGRHIYIY 120

QY 121 VPPDPVAFPLGMDYLVIVEDDSDAIIPCRITDPTPTVTLHNSGVWPASVDSROGFGNG 180
DB 121 VPPDPVAFPLGMDYLVIVEDDSDAIIPCRITDPTPTVTLHNSGVWPASVDSROGFGNG 180

QY 181 TFTVGPYICBATVKGKFKQTPINPVVALKATSELDLEMAKLTVYKSGETIVVTCVAFNN 240
DB 181 TFTVGPYICBATVKGKFKQTPINPVVALKATSELDLEMAKLTVYKSGETIVVTCVAFNN 240

QY 241 EVVDLQWTPGEVKGKGTMLBEIKVPSIKLVTLVPEATVKDSDGYECAARQATREVK 300
DB 241 EVVDLQWTPGEVKGKGTMLBEIKVPSIKLVTLVPEATVKDSDGYECAARQATREVK 300

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QY 301 EMKKVTVISVHEKGFIEIKPTFSQLEAVNLHVKHFVVEVRAVPPPRISWLKNNLTIIENL 360
DB 301 EMKKVTVISVHEKGFIEIKPTFSQLEAVNLHVKHFVVEVRAVPPPRISWLKNNLTIIENL 360

QY 361 TEITTDVEKIOEIRYRSKLLIIRAKEEDSGHYTIIVAQNEDAVKSYTFELLTQVPSIIDL 420
DB 361 TEITTDVEKIOEIRYRSKLLIIRAKEEDSGHYTIIVAQNEDAVKSYTFELLTQVPSIIDL 420

QY 421 VDDHGSTGGQTVRCRTAEGTPLDIEWMIKCDIKKCNNETSWTILANNVSNITTEIHSRD 480
DB 421 VDDHGSTGGQTVRCRTAEGTPLDIEWMIKCDIKKCNNETSWTILANNVSNITTEIHSRD 480

QY 481 RSTVEGRVTFKAVEETIAVRCLAKNLLGAENRELKLVAPTLSRSELTVAAAVLLVIVII 540
DB 481 RSTVEGRVTFKAVEETIAVRCLAKNLLGAENRELKLVAPTLSRSELTVAAAVLLVIVII 540

QY 541 SLIIVLVIIWKQPRYRIRWRVIESISPDGHEIYYDPMQLPYDSRWEFFRDPGLVLRGLG 600
DB 541 SLIIVLVIIWKQPRYRIRWRVIESISPDGHEIYYDPMQLPYDSRWEFFRDPGLVLRGLG 600

QY 601 SGAFGKVVGSTAYGLSRSQPVKMAVVKMLKPTARSSEKQALMSELKIMTHLGHPLNIVNL 660
DB 601 SGAFGKVVGSTAYGLSRSQPVKMAVVKMLKPTARSSEKQALMSELKIMTHLGHPLNIVNL 660

QY 661 LGACTKSGPIYIITEYCFYGDVNLVHLKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720
DB 661 LGACTKSGPIYIITEYCFYGDVNLVHLKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720

QY 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSIDTQSLYDRPASYKKKSMMLDSEVKN 780
DB 721 VILSFENNGDYMDKQADTTQYVPMLEKEVSKYSIDTQSLYDRPASYKKKSMMLDSEVKN 780

QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840
DB 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840

QY 841 RDIHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900
DB 841 RDIHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900

QY 901 VDSFTFNKIKSGYRMKPDPHATSEVVEIMVKWNSPEKPSFYHLSEIVENLLPGQYKK 960
DB 901 VDSFTFNKIKSGYRMKPDPHATSEVVEIMVKWNSPEKPSFYHLSEIVENLLPGQYKK 960

QY 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII 1020
DB 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII 1020

QY 1021 PLPDIDPVEEDLGRNHRSSQTSSESAIETGSSSTFIKREDETIEDIMMDDIGIDS 1080
DB 1021 PLPDIDPVEEDLGRNHRSSQTSSESAIETGSSSTFIKREDETIEDIMMDDIGIDS 1080

QY 1081 SDLVEDSFL 1089
DB 1081 SDLVEDSFL 1089

RESULT 8
US-10-741-601-439
; Sequence 439, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 439
; LENGTH: 1089
; TYPE: PRT

```

Db	961	SYEKIHLDFLKSDHPAVARVRVSDNAYIGVYTKNEEDKLDKDWEGGLDEQRLSADSGYII	1020
Qy	1021	PLPDIDVPPEEDLGKRNHRSSQTSSESAITGSSSTFFIKREDETIEDIDMDDIGIDS	1080
Db	1021	PLPDIDVPPEEDLGKRNHRSSQTSSESAITGSSSTFFIKREDETIEDIDMDDIGIDS	1080
Qy	1081	SDLVEDSFL	1089
Db	1081	SDLVEDSFL	1089
<p>RESULT 9</p> <p>US-10-741-600-1304</p> <p>; Sequence 1304, Application US/10741600</p> <p>; Publication No. US20050026169A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: CARGILL, Michele et al.</p> <p>; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF</p> <p>; FILE REFERENCE: CL001499</p> <p>; CURRENT APPLICATION NUMBER: US/10741.600</p> <p>; CURRENT FILING DATE: 2003-12-22</p> <p>; NUMBER OF SEQ ID NOS: 73997</p> <p>; SOFTWARE: FastSeq for Windows Version 4.0</p> <p>; SEQ ID NO 1304</p> <p>; LENGTH: 1089</p> <p>; TYPE: PRT</p> <p>; ORGANISM: Homo sapiens</p> <p>US-10-741-600-1304</p>			
<p>Query Match 100.0%; Score 5652; DB 17; Length 1089;</p> <p>Best Local Similarity 100.0%; Pred. No. 1.2e-311;</p> <p>Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>			
Qy	1	MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNENEKVVQLNSSFSRLRCFGESEVSWQYP	60
Db	1	MGTSHPAFLVLGCLLTGLSLILCOLSLPSILPNENEKVVQLNSSFSRLRCFGESEVSWQYP	60
Qy	61	MSEESSDVEIRNEBNNSGLFVTVLEVSSASAAHTGLTYCYNNHTQTENELEGRHIYIY	120
Db	61	MSEESSDVEIRNEBNNSGLFVTVLEVSSASAAHTGLTYCYNNHTQTENELEGRHIYIY	120
Qy	121	VPDPDVAFLPGMTDYLVIVVEDDSSAII PCRTTDPETPTVLHNSGCVVPASYDSRQGFNG	180
Db	121	VPDPDVAFLPGMTDYLVIVVEDDSSAII PCRTTDPETPTVLHNSGCVVPASYDSRQGFNG	180
Qy	181	TFTVGPYICATVKGKGFQTI PFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
Db	181	TFTVGPYICATVKGKGFQTI PFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
Qy	241	EVVDLOWTYPEGVKGGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
Db	241	EVVDLOWTYPEGVKGGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK	300
Qy	301	EMKQVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP PPRISLWKNLTLIENL	360
Db	301	EMKQVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP PPRISLWKNLTLIENL	360
Qy	361	TEITTDVEKIQEIYRSKLLIRAKESDSGHYTTVAQNEADAVKSVTFPELLTQVPSILLDL	420
Db	361	TEITTDVEKIQEIYRSKLLIRAKESDSGHYTTVAQNEADAVKSVTFPELLTQVPSILLDL	420
Qy	421	VDDHGGSTGGQVRCCTAEGTPLPDIEWMI CKDIKKCNNETSWTILANNVSNII TEIHSRD	480
Db	421	VDDHGGSTGGQVRCCTAEGTPLPDIEWMI CKDIKKCNNETSWTILANNVSNII TEIHSRD	480
Qy	481	RSTVEGRVTFPAKVEETIAVRCLAKNVLGAENRELKLVAPTLRSELTVAAAVLLVLVII	540
Db	481	RSTVEGRVTFPAKVEETIAVRCLAKNVLGAENRELKLVAPTLRSELTVAAAVLLVLVII	540
Qy	541	SLIVLVVIMFQKPYEIRWRVIESISPDGHEIYIYVDPQMLPYDSRWEPPRDLGLVLRVLG	600
Db	541	SLIVLVVIMFQKPYEIRWRVIESISPDGHEIYIYVDPQMLPYDSRWEPPRDLGLVLRVLG	600

QY 601 SGAFKVECTAYCISRSQPMKAVKMLKPTARSSEKQALMSLKIIMTHLGHPLNIVNL 660  
 DB 601 SGAFKVECTAYCISRSQPMKAVKMLKPTARSSEKQALMSLKIIMTHLGHPLNIVNL 660  
 QY 661 LGACTKSGPIIITEYCFYGDVNLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
 DB 661 LGACTKSGPIIITEYCFYGDVNLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
 QY 721 VILSFENNNDYMDKQADTTQYVPMLEKEVSKYSDIORSLYDRPASYYKKSMLDSEVKXN 780  
 DB 721 VILSFENNNDYMDKQADTTQYVPMLEKEVSKYSDIORSLYDRPASYYKKSMLDSEVKXN 780  
 QY 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840  
 DB 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840  
 QY 841 RDIMHDSNYVSKGSTPLPVKWMAPESIFDNLYTTLSDVMSYIGILLWEIFSLGGTYPYGMW 900  
 DB 841 RDIMHDSNYVSKGSTPLPVKWMAPESIFDNLYTTLSDVMSYIGILLWEIFSLGGTYPYGMW 900  
 QY 901 VDSFTFNKIKSGYRMKPDHATSEVTEIMVKWCNSEPEKPSFYHLSEIVENLLPGQYKK 960  
 DB 901 VDSFTFNKIKSGYRMKPDHATSEVTEIMVKWCNSEPEKPSFYHLSEIVENLLPGQYKK 960  
 QY 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTKNEEDKLKOWEGGLDEORLSADSXYII 1020  
 DB 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTKNEEDKLKOWEGGLDEORLSADSXYII 1020  
 QY 1021 PLPDIDPVEEDLGKRNHSSQTSESAIETGSSSTFIKREDETIEDIMDDIGIDS 1080  
 DB 1021 PLPDIDPVEEDLGKRNHSSQTSESAIETGSSSTFIKREDETIEDIMDDIGIDS 1080  
 QY 1081 SLDVEDSFL 1089  
 DB 1081 SLDVEDSFL 1089

RESULT 10  
 US-09-866-510-10  
 ; Sequence 10, Application US/09866510  
 ; Patent No. US20020111304A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KAZLAUSKAS, ANDRIUS  
 ; APPLICANT: IKUNO, YASUSHI  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES  
 ; FILE REFERENCE: ERM-104.01  
 ; CURRENT APPLICATION NUMBER: US/09/866, 510  
 ; CURRENT FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: 60/250,747  
 ; PRIOR FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: 60/289,103  
 ; PRIOR FILING DATE: 2001-05-07  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 10  
 ; LENGTH: 1089  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-866-510-10

Query Match 99.9%; Score 5649; DB 9; Length 1089;  
 Best Local Similarity 99.9%; Pred. No. 1.8e-311;  
 Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVLCGLLGLSLILCOLSLPILPNEKVVQLNSSFILRCFGESEVSWQYP 60  
 DB 1 MGTSHPAFLVLCGLLGLSLILCOLSLPILPNEKVVQLNSSFILRCFGESEVSWQYP 60  
 QY 61 MSEEESDVEIRNEENNSGLFTVLEVSASAAHTGLTYCYNHTQTENELEGRHIYIY 120  
 DB 61 MSEEESDVEIRNEENNSGLFTVLEVSASAAHTGLTYCYNHTQTENELEGRHIYIY 120

QY 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITTDPTPTVTLHNSGVVPASVDSROGFNG 180  
 DB 121 VPDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITTDPTPTVTLHNSGVVPASVDSROGFNG 180  
 QY 181 TPTVGPYICAEATVKGKKFOTIPFNVYALKATSELDLEMEALKTVYKSGGTIVVTCVAFNN 240  
 DB 181 TPTVGPYICAEATVKGKKFOTIPFNVYALKATSELDLEMEALKTVYKSGGTIVVTCVAFNN 240  
 QY 241 EVVDLOWTYPGEVKGKIGITMLBEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300  
 DB 241 EVVDLOWTYPGEVKGKIGITMLBEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300  
 QY 301 EMKKTVISVHEKGFTEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRI SWLKNLTLIENL 360  
 DB 301 EMKKTVISVHEKGFTEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRI SWLKNLTLIENL 360  
 QY 361 TEITTDVEKIQBIYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420  
 DB 361 TEITTDVEKIQBIYRSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420  
 QY 421 VDDHGSTGGQVTRCTAEGTPLPDIEWMICKDOKKCNNETSWTILANNYSNIIITEHSRD 480  
 DB 421 VDDHGSTGGQVTRCTAEGTPLPDIEWMICKDOKKCNNETSWTILANNYSNIIITEHSRD 480  
 QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540  
 DB 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLVIVII 540  
 QY 541 SLIIVLVIMWKPRYEIRWRVIESIPDGHEIYIYDPMOLPYDSRWEFPRDGLVLRVLG 600  
 DB 541 SLIIVLVIMWKPRYEIRWRVIESIPDGHEIYIYDPMOLPYDSRWEFPRDGLVLRVLG 600  
 QY 601 SGAFKVECTAYCISRSQPMKAVKMLKPTARSSEKQALMSLKIIMTHLGHPLNIVNL 660  
 DB 601 SGAFKVECTAYCISRSQPMKAVKMLKPTARSSEKQALMSLKIIMTHLGHPLNIVNL 660  
 QY 661 LGACTKSGPIIITEYCFYGDVNLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
 DB 661 LGACTKSGPIIITEYCFYGDVNLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
 QY 721 VILSFENNNDYMDKQADTTQYVPMLEKEVSKYSDIORSLYDRPASYYKKSMLDSEVKXN 780  
 DB 721 VILSFENNNDYMDKQADTTQYVPMLEKEVSKYSDIORSLYDRPASYYKKSMLDSEVKXN 780  
 QY 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840  
 DB 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840  
 QY 841 RDIMHDSNYVSKGSTPLPVKWMAPESIFDNLYTTLSDVMSYIGILLWEIFSLGGTYPYGMW 900  
 DB 841 RDIMHDSNYVSKGSTPLPVKWMAPESIFDNLYTTLSDVMSYIGILLWEIFSLGGTYPYGMW 900  
 QY 901 VDSFTFNKIKSGYRMKPDHATSEVTEIMVKWCNSEPEKPSFYHLSEIVENLLPGQYKK 960  
 DB 901 VDSFTFNKIKSGYRMKPDHATSEVTEIMVKWCNSEPEKPSFYHLSEIVENLLPGQYKK 960  
 QY 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTKNEEDKLKOWEGGLDEORLSADSXYII 1020  
 DB 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTKNEEDKLKOWEGGLDEORLSADSXYII 1020  
 QY 1021 PLPDIDPVEEDLGKRNHSSQTSESAIETGSSSTFIKREDETIEDIMDDIGIDS 1080  
 DB 1021 PLPDIDPVEEDLGKRNHSSQTSESAIETGSSSTFIKREDETIEDIMDDIGIDS 1080  
 QY 1081 SLDVEDSFL 1089  
 DB 1081 SLDVEDSFL 1089

RESULT 11  
 US-09-866-510-4  
 ; Sequence 4, Application US/09866510  
 ; Patent No. US20020111304A1

GENERAL INFORMATION:	
APPLICANT:	KAZLAUSKAS, ANDRIUS
FILE OF INVENTION:	IKUNO, YASUSHI
TITLE OF INVENTION:	METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
FILE REFERENCE:	ERM-104.01
CURRENT APPLICATION NUMBER:	US/09/866,510
CURRENT FILING DATE:	2001-05-25
PRIOR APPLICATION NUMBER:	60/250,747
PRIOR FILING DATE:	2000-12-01
PRIOR APPLICATION NUMBER:	60/289,103
PRIOR FILING DATE:	2001-05-07
NUMBER OF SEQ ID NOS:	33
SOFTWARE:	Patent In Ver. 2.1
SEQ ID NO 4	
LENGTH:	1089
TYPE:	PRT
ORGANISM:	Homo sapiens
US-09-866-510-4	
Query Match 99.9%; Score 5648; DB 9; Length 1089;	
Best Local Similarity 99.9%; Pred. No. 2.le-311;	
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MGTSHPAFLVLGCLLTGLSLILQCLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60
DB	1 MGTSHPAFLVLGCLLTGLSLILQCLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60
QY	61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNNHTOTENELEGRHIYI 120
DB	61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNNHTOTENELEGRHIYI 120
QY	121 VPDVDAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVPAVSDYSDRGFNG 180
DB	121 VPDVDAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVPAVSDYSDRGFNG 180
QY	181 TPTVGPYICATVKGKFKQTPINPVNVALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
DB	181 TPTVGPYICATVKGKFKQTPINPVNVALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
QY	241 EVVDLQWTVPGVKGKGTMLBEIKVPSIKLVTLTVPEATVKDSDGYCAARQATREV 300
DB	241 EVVDLQWTVPGVKGKGTMLBEIKVPSIKLVTLTVPEATVKDSDGYCAARQATREV 300
QY	301 EMKKVTISVHEKGFBIKPTFSQLEAVNLHVEKHFVVEVRAVPPRISMLKNLTLIENL 360
DB	301 EMKKVTISVHEKGFBIKPTFSQLEAVNLHVEKHFVVEVRAVPPRISMLKNLTLIENL 360
QY	361 TEITDVEKIQEIYRYSKULIRAKBEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
DB	361 TEITDVEKIQEIYRYSKULIRAKBEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
QY	421 VDDHGSTGCTGCTVCTAEGTLPDIEWMICKDKKCNNETSWTILANNYSNIITEIHSRD 480
DB	421 VDDHGSTGCTGCTVCTAEGTLPDIEWMICKDKKCNNETSWTILANNYSNIITEIHSRD 480
QY	481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLSRELTVAAAVLVLLVIVII 540
DB	481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLSRELTVAAAVLVLLVIVII 540
QY	541 SLIVLVVWVKQKPYEIRNRVIESISPDGHEIYIVDPMDQLPYDSRWEPRDGLVLRVLG 600
DB	541 SLIVLVVWVKQKPYEIRNRVIESISPDGHEIYIVDPMDQLPYDSRWEPRDGLVLRVLG 600
QY	601 SGAFGKVGVEGTAYGLSRQPMVKVAVKMLKPTARSSEKQALMSELKIMTHLGHPLNIVNL 660
DB	601 SGAFGKVGVEGTAYGLSRQPMVKVAVKMLKPTARSSEKQALMSELKIMTHLGHPLNIVNL 660
QY	661 LGACTKSGPIYIITEYCFYGDVLYNLHKNRDSFLSHHPKPKKELDI FGLNPADESTRSY 720
DB	661 LGACTKSGPIYIITEYCFYGDVLYNLHKNRDSFLSHHPKPKKELDI FGLNPADESTRSY 720
QY	721 VILSPENNGDYMDKQADTTQYVPMLEKRVSKYSDIQRSLYDRPASYYKKSKMLDSEVKY 780
DB	721 VILSPENNGDYMDKQADTTQYVPMLEKRVSKYSDIQRSLYDRPASYYKKSKMLDSEVKY 780

Db	721	VILSPENNGDYMDKQADTTQYVPMLEKRVSKYSDIQRSLYDRPASYYKKSKMLDSEVKY	780
QY	781	LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
QY	841	ROIIMHDSNVVSKGSTPLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM	900
Db	841	ROIIMHDSNVVSKGSTPLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM	900
QY	901	VDSFTFYNKIKSGYRMAKPDHATSEVYIIMVKWCNSEPEKRPSPSYHLSEIVENLLPGQYK	960
Db	901	VDSFTFYNKIKSGYRMAKPDHATSEVYIIMVKWCNSEPEKRPSPSYHLSEIVENLLPGQYK	960
QY	961	SYEKIHLDFLKSDHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII	1020
Db	961	SYEKIHLDFLKSDHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII	1020
QY	1021	PLPDIDPVPEEDLGRNHRHSQTSESAIETGSSSSTFIKREDETIEDIMMDDIGIDS	1080
Db	1021	PLPDIDPVPEEDLGRNHRHSQTSESAIETGSSSSTFIKREDETIEDIMMDDIGIDS	1080
QY	1081	SDLVEDSFL 1089	
Db	1081	SDLVEDSFL 1089	
RESULT 12			
US-09-955-363-36			
Sequence 36, Application US/09955363			
Patent No. US20020173621A1			
GENERAL INFORMATION:			
APPLICANT: Sledziewski Ph.D., Andrzej Z			
Bell, Lillian A.			
Kindvogel Ph.D., Wayne R.			
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS			
AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE			
FUSIONS			
NUMBER OF SEQUENCES: 36			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Seed and Berry			
STREET: 6300 Columbia Center			
CITY: Seattle			
STATE: WA			
COUNTRY: USA			
ZIP: 98104-7092			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent In Release #1.24			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/955,363			
FILING DATE: 18-Sep-2001			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/634,510			
FILING DATE: <Unknown>			
APPLICATION NUMBER: US 07/347,291			
FILING DATE: 02-MAY-1989			
ATTORNEY/AGENT INFORMATION:			
NAME: Maki J.D., David J.			
REGISTRATION NUMBER: 31,392			
REFERENCE/DOCKET NUMBER: 990008.446C3			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 206-622-4900			
TELEFAX: 206-682-6031			
TELEX: 3723836			
INFORMATION FOR SEQ ID NO: 36:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1089 amino acids			
TYPE: amino acid			
TOPOLOGY: linear			

MOLECULE TYPE: protein		SEQUENCE DESCRIPTION: SEQ ID NO: 36:	
; US-09-955-363-36			
Query Match		99.9%; Score 5648; DB 9; Length 1089;	
Best Local Similarity		99.9%; Pred. No. 2.1e-311;	
Matches 1089; Conservative		1; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MGTSHPAFLVGLCLLTGLSLILCOLSLPILPNEKVKVQLNSFSRLRCFGESEVSWQYP	60
DB	1	MGTSHPAFLVGLCLLTGLSLILCOLSLPILPNEKVKVQLNSFSRLRCFGESEVSWQYP	60
QY	61	MSEESSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENLEGRHIYI	120
DB	61	MSEESSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENLEGRHIYI	120
QY	121	VPDPVAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASYSRQGFNG	180
DB	121	VPDPVAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASYSRQGFNG	180
QY	181	TFTVGPYICEATVKGKFKQTIIPNVYALKATSELDLEMEALKTVYKSGETIVTCAVFN	240
DB	181	TFTVGPYICEATVKGKFKQTIIPNVYALKATSELDLEMEALKTVYKSGETIVTCAVFN	240
QY	241	EVVDLQWTVPEGVKGGITLLEIKVPSIKLVTVLTPVPEATVKDGDYECARQATREV	300
DB	241	EVVDLQWTVPEGVKGGITLLEIKVPSIKLVTVLTPVPEATVKDGDYECARQATREV	300
QY	301	EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVHFVVEVRAYPPIRISMLKNNLTLE	360
DB	301	EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVHFVVEVRAYPPIRISMLKNNLTLE	360
QY	361	TEITTDVEKIQIRYRSKLIIRAKEEDSGHYTIVAQNEADVKS YTFELLTQVPSILDL	420
DB	361	TEITTDVEKIQIRYRSKLIIRAKEEDSGHYTIVAQNEADVKS YTFELLTQVPSILDL	420
QY	421	VDDHSGTGQVRCVTAEGTLPDIEMWICKDKKCNNETSWTILANNVSNITIEHSRD	480
DB	421	VDDHSGTGQVRCVTAEGTLPDIEMWICKDKKCNNETSWTILANNVSNITIEHSRD	480
QY	481	RSTVEGRVTFPAKVETIAVRCIAKNNLGAENRELKVAPTLRSELVAAAVLVIVII	540
DB	481	RSTVEGRVTFPAKVETIAVRCIAKNNLGAENRELKVAPTLRSELVAAAVLVIVII	540
QY	541	SLVLVVIWKQKPRYERIRNRVIESIPDGHXYIYVDPMLPYDSRWEFFRDGLVGRVL	600
DB	541	SLVLVVIWKQKPRYERIRNRVIESIPDGHXYIYVDPMLPYDSRWEFFRDGLVGRVL	600
QY	601	SGAFKVVVECTAYGLSRQSPVMKVAVKMLKPTARSSEKQALMSSELKIMTHLGP	660
DB	601	SGAFKVVVECTAYGLSRQSPVMKVAVKMLKPTARSSEKQALMSSELKIMTHLGP	660
QY	661	LGACTKSGPIYIITEYCFYGDLYNLYHKNRDPSLHHPKPKKELDI FGLNPADESTR	720
DB	661	LGACTKSGPIYIITEYCFYGDLYNLYHKNRDPSLHHPKPKKELDI FGLNPADESTR	720
QY	721	VILSFENNGDMDKQADTQYVPMLEKEVSKYSDIQSLYDRPAS YKKKMLDSEVKN	780
DB	721	VILSFENNGDMDKQADTQYVPMLEKEVSKYSDIQSLYDRPAS YKKKMLDSEVKN	780
QY	781	LLSDDNSEGTLTDLDSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDF	840
DB	781	LLSDDNSEGTLTDLDSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDF	840
QY	841	RDIMHDSNVYKSGTFLPVKWMAPESIFDNLTYTLLSDVMSYGTILLWEISLGGT	900
DB	841	RDIMHDSNVYKSGTFLPVKWMAPESIFDNLTYTLLSDVMSYGTILLWEISLGGT	900
QY	901	VDSFTFNKIKSGYRMKPDPHATSEVVEIMVKNSEPEKRPSPYHLSEIVENLLPQYK	960
DB	901	VDSFTFNKIKSGYRMKPDPHATSEVVEIMVKNSEPEKRPSPYHLSEIVENLLPQYK	960
QY	961	SYEKIHLDFLKSHPAVARWVDSNAYIGVTYKNEEDKLKOWEGGLDQRLSADSGYII	1020
DB	961	SYEKIHLDFLKSHPAVARWVDSNAYIGVTYKNEEDKLKOWEGGLDQRLSADSGYII	1020
QY	1021	PLPDDIDPVEEEDLGRNRHSSQTSESAIETGSSSSTFIKREDETIEDIMMDDIGIDS	1080
DB	1021	PLPDDIDPVEEEDLGRNRHSSQTSESAIETGSSSSTFIKREDETIEDIMMDDIGIDS	1080
QY	1081	SDLVEDSFL 1089	
DB	1081	SDLVEDSFL 1089	
RESULT 13			
US-09-866-510-8			
; Sequence 8, Application US/09866510			
; Patent No. US20020111304A1			
; GENERAL INFORMATION:			
; APPLICANT: KAZLAUSKAS, ANDRIUS			
; APPLICANT: IKUNO, YASUSHI			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES			
; FILE REFERENCE: ERM-104.01			
; CURRENT APPLICATION NUMBER: US/09/866,510			
; CURRENT FILING DATE: 2001-05-25			
; PRIOR APPLICATION NUMBER: 60/250,747			
; PRIOR FILING DATE: 2000-12-01			
; PRIOR APPLICATION NUMBER: 60/289,103			
; PRIOR FILING DATE: 2001-05-07			
; NUMBER OF SEQ ID NOS: 33			
; SOFTWARE: Patent In Ver. 2.1			
; SEQ ID NO 8			
; LENGTH: 1089			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-866-510-8			
Query Match		99.9%; Score 5647; DB 9; Length 1089;	
Best Local Similarity		99.9%; Pred. No. 2.3e-311;	
Matches 1089; Conservative		1; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MGTSHPAFLVGLCLLTGLSLILCOLSLPILPNEKVKVQLNSFSRLRCFGESEVSWQYP	60
DB	1	MGTSHPAFLVGLCLLTGLSLILCOLSLPILPNEKVKVQLNSFSRLRCFGESEVSWQYP	60
QY	61	MSEESSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENLEGRHIYI	120
DB	61	MSEESSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENLEGRHIYI	120
QY	121	VPDPVAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASYSRQGFNG	180
DB	121	VPDPVAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASYSRQGFNG	180
QY	181	TFTVGPYICEATVKGKFKQTIIPNVYALKATSELDLEMEALKTVYKSGETIVTCAVFN	240
DB	181	TFTVGPYICEATVKGKFKQTIIPNVYALKATSELDLEMEALKTVYKSGETIVTCAVFN	240
QY	241	EVVDLQWTVPEGVKGGITLLEIKVPSIKLVTVLTPVPEATVKDGDYECARQATREV	300
DB	241	EVVDLQWTVPEGVKGGITLLEIKVPSIKLVTVLTPVPEATVKDGDYECARQATREV	300
QY	301	EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVHFVVEVRAYPPIRISMLKNNLTLE	360
DB	301	EMKKTIVSVHEKGFIEIKPTFSQLEAVNLHEVHFVVEVRAYPPIRISMLKNNLTLE	360
QY	361	TEITTDVEKIQIRYRSKLIIRAKEEDSGHYTIVAQNEADVKS YTFELLTQVPSILDL	420
DB	361	TEITTDVEKIQIRYRSKLIIRAKEEDSGHYTIVAQNEADVKS YTFELLTQVPSILDL	420
QY	421	VDDHSGTGQVRCVTAEGTLPDIEMWICKDKKCNNETSWTILANNVSNITIEHSRD	480
DB	421	VDDHSGTGQVRCVTAEGTLPDIEMWICKDKKCNNETSWTILANNVSNITIEHSRD	480
QY	481	RSTVEGRVTFPAKVETIAVRCIAKNNLGAENRELKVAPTLRSELVAAAVLVIVII	540
DB	481	RSTVEGRVTFPAKVETIAVRCIAKNNLGAENRELKVAPTLRSELVAAAVLVIVII	540

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Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540
QY 541 SLILVVIWKQPRYIRVRVIESISPDGHEIYYVDPMLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLILVVIWKQPRYIRVRVIESISPDGHEIYYVDPMLPYDSRWEFPRDGLVLRVLG 600
QY 601 SGAFKVGVTAYGLSRSPQVMKVAVKMLKPTARSSEKQALMSSELKIMTHLGPLHNL 660
Db 601 SGAFKVGVTAYGLSRSPQVMKVAVKMLKPTARSSEKQALMSSELKIMTHLGPLHNL 660
QY 661 LGACTKSGPIIYITEYCFYGDVLYLHKNRDPSLHHPKPKKELDI FGLNPADESTSY 720
Db 661 LGACTKSGPIIYITEYCFYGDVLYLHKNRDPSLHHPKPKKELDI FGLNPADESTSY 720
QY 721 VILSPENNGDYMDKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMLDSEVK 780
Db 721 VILSPENNGDYMDKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMLDSEVK 780
QY 781 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQOKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQOKIVKICDFGLA 840
QY 841 RDIMHDSNVYSGSTFLPVKNWAPESIFDNLYTTLSDVMSYGILLWEI FSLGTPPGMM 900
Db 841 RDIMHDSNVYSGSTFLPVKNWAPESIFDNLYTTLSDVMSYGILLWEI FSLGTPPGMM 900
QY 901 VDSFTFVNKIKSGYRMAKPDHATSEVYIMVKWNSPEKRPSPFYHLSEI VENLLPGQYKK 960
Db 901 VDSFTFVNKIKSGYRMAKPDHATSEVYIMVKWNSPEKRPSPFYHLSEI VENLLPGQYKK 960
QY 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTVYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTVYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
QY 1021 PLPDDIPVPEEEDLGKRNHSSQTSESAIETGSSSSTFIKREDETI EDIDMDDDGIDS 1080
Db 1021 PLPDDIPVPEEEDLGKRNHSSQTSESAIETGSSSSTFIKREDETI EDIDMDDDGIDS 1080
QY 1081 SDLVDSFL 1089
Db 1081 SDLVDSFL 1089

RESULT 14
US-09-866-510-6
; Sequence 6, Application US/09866510
; Patent No. US20020113041
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-6

Query Match 99.9%; Score 5646; DB 9; Length 1089;
Best Local Similarity 99.9%; Pred. No. 2.7e-311;
Matches 1088; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVLCGLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60
Db 1 MGTSHPAFLVLCGLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db 61 MSEEESDVEIRNEENNNSGLFVTLLEVSSASAAHTGLTYCYNHTQTBEENLEGRHIYI 120
QY 121 VPDPOVAFVPLGMDTYLVIVEDDDSAIIPCRRTDPTPTVTLHNSGVVPASYSRQGFNG 180
Db 121 VPDPOVAFVPLGMDTYLVIVEDDDSAIIPCRRTDPTPTVTLHNSGVVPASYSRQGFNG 180
QY 181 TTTVGPYICEATVKGKGFOTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
Db 181 TTTVGPYICEATVKGKGFOTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
QY 241 EYVDLQWTPYGEVKGKGIITMLEEIKVPSIKLYVTTLVTPBATVKDSDGYECAARQATREV 300
Db 241 EYVDLQWTPYGEVKGKGIITMLEEIKVPSIKLYVTTLVTPBATVKDSDGYECAARQATREV 300
QY 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVKHFVVEVRAYPPPRISMLKNNLTILENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVKHFVVEVRAYPPPRISMLKNNLTILENL 360
QY 361 TEITTDVEKIQIRYRSKLKIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQIRYRSKLKIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
QY 421 VDDHGSTGGQVTRCTAEGTLPDIEWMI CKDIKKCNNETSWTILANNYSNIITEIHSRD 480
Db 421 VDDHGSTGGQVTRCTAEGTLPDIEWMI CKDIKKCNNETSWTILANNYSNIITEIHSRD 480
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540
QY 541 SLILVVIWKQPRYIRVRVIESISPDGHEIYYVDPMLPYDSRWEFPRDGLVLRVLG 600
Db 541 SLILVVIWKQPRYIRVRVIESISPDGHEIYYVDPMLPYDSRWEFPRDGLVLRVLG 600
QY 601 SGAFKVGVTAYGLSRSPQVMKVAVKMLKPTARSSEKQALMSSELKIMTHLGPLHNL 660
Db 601 SGAFKVGVTAYGLSRSPQVMKVAVKMLKPTARSSEKQALMSSELKIMTHLGPLHNL 660
QY 661 LGACTKSGPIIYITEYCFYGDVLYLHKNRDPSLHHPKPKKELDI FGLNPADESTSY 720
Db 661 LGACTKSGPIIYITEYCFYGDVLYLHKNRDPSLHHPKPKKELDI FGLNPADESTSY 720
QY 721 VILSPENNGDYMDKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMLDSEVK 780
Db 721 VILSPENNGDYMDKQADTTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKSMLDSEVK 780
QY 781 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQOKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQOKIVKICDFGLA 840
QY 841 RDIMHDSNVYSGSTFLPVKNWAPESIFDNLYTTLSDVMSYGILLWEI FSLGTPPGMM 900
Db 841 RDIMHDSNVYSGSTFLPVKNWAPESIFDNLYTTLSDVMSYGILLWEI FSLGTPPGMM 900
QY 901 VDSFTFVNKIKSGYRMAKPDHATSEVYIMVKWNSPEKRPSPFYHLSEI VENLLPGQYKK 960
Db 901 VDSFTFVNKIKSGYRMAKPDHATSEVYIMVKWNSPEKRPSPFYHLSEI VENLLPGQYKK 960
QY 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTVYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTVYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
QY 1021 PLPDDIPVPEEEDLGKRNHSSQTSESAIETGSSSSTFIKREDETI EDIDMDDDGIDS 1080
Db 1021 PLPDDIPVPEEEDLGKRNHSSQTSESAIETGSSSSTFIKREDETI EDIDMDDDGIDS 1080
QY 1081 SDLVDSFL 1089
Db 1081 SDLVDSFL 1089
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RESULT 15
US-09-961-403-4
; Sequence 4, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-4

Query Match          99.7%; Score 5636.5; DB 10; Length 1088;
Best Local Similarity 99.9%; Pred. No. 9.2e-311;
Matches 1088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPLPNEKVKVQLNSSFSLRCFGESEVSNQYP 60
Db 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPLPNEKVKVQLNSSFSLRCFGESEVSNQYP 60

Qy 61 MSSEESDVEIRNEENNSGIFVTVLEVSSASAHTGLTYCYNHTQTEENLEGRHIYIY 120
Db 61 MSSEESDVEIRNEENNSGIFVTVLEVSSASAHTGLTYCYNHTQTEENLEGRHIYIY 120

Qy 121 VPDPDAFVPLGMDYLVIVEDDDSAIIPCRITTDPTPTVTLHNSGVVPASYSRQGFNG 180
Db 121 VPDPDAFVPLGMDYLVIVEDDDSAIIPCRITTDPTPTVTLHNSGVVPASYSRQGFNG 180

Qy 181 TPTVGPYICBATVKGKGFQIIPNVVALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
Db 181 TPTVGPYICBATVKGKGFQIIPNVVALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240

Qy 241 EVVDLQWTPGEVKGKGIITMLEIKVPSIKLVVTLVPEATVKDSDGYECAARQATREVK 300
Db 241 EVVDLQWTPGEVKGKGIITMLEIKVPSIKLVVTLVPEATVKDSDGYECAARQATREVK 300

Qy 301 EMKKTIVSHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISMKNLTLIENL 360
Db 301 EMKKTIVSHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISMKNLTLIENL 360

Qy 361 TEITTDVEKIQEIRYSKLIIRAKEDSGHYITVAQNEADAVKSYTFELLTQVPSSILD 420
Db 361 TEITTDVEKIQEIRYSKLIIRAKEDSGHYITVAQNEADAVKSYTFELLTQVPSSILD 420

Qy 421 VDDHGSTGGQVRCVTAEGTLPDIEWMICKIKKNNETSWTILANNYSNIITEIHSRD 480
Db 421 VDDHGSTGGQVRCVTAEGTLPDIEWMICKIKKNNETSWTILANNYSNIITEIHSRD 480

Qy 481 RSTVEGRVTFPAKVEETIAVRCLAKNLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db 481 RSTVEGRVTFPAKVEETIAVRCLAKNLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy 541 SLIVAVVINKQKPRYRIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFRDGLVLRVLG 600
Db 541 SLIVAVVINKQKPRYRIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFFRDGLVLRVLG 600

Qy 601 SGAFGKVEGTAYGLSRQPMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNLVNL 660
Db 601 SGAFGKVEGTAYGLSRQPMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNLVNL 660

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Search completed: March 11, 2005, 07:53:00  
Job time : 77.9307 secs

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Db 661 LGACTKSGPIYIIITEYCFYGDLVNLYLHKNRDSFLSHHPKPKKELDI FGLNPADESTSY 720

Qy 721 VILSFENNNGDYMDMKQADTTQYVPMLEKREVSYSIDIQRSLYDRPASYYKKSKMLDSEVKN 780
Db 721 VILSFENNNGDYMDMKQADTTQYVPMLEKREVSYSIDIQRSLYDRPASYYKKSKMLDSEVKN 780

Qy 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840

Qy 841 RDIMHDSNVVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900
Db 841 RDIMHDSNVVSKGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900

Qy 901 VDSFTYFKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSPFYHLSEIVENLLPQYKK 960
Db 901 VDSFTYFKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSPFYHLSEIVENLLPQYKK 960

Qy 961 SYEKIHLDFLKSDHPAVARMVDSNAYIGVTYKNEEDKLKOWEGGLDQRLSADSGYII 1020
Db 961 SYEKIHLDFLKSDHPAVARM-VDSNAYIGVTYKNEEDKLKOWEGGLDQRLSADSGYII 1019

Qy 1021 PLPDI DPVEEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMDDDIGDS 1080
Db 1020 PLPDI DPVEEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMDDDIGDS 1079

Qy 1081 SOLVEDSFL 1089
Db 1080 SOLVEDSFL 1088

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2005, 04:13:19 ; Search time 127.505 Seconds  
(without alignments)  
3303.265 Million cell updates/sec

Title: US-10-027-400-2

Perfect score: 5652

Sequence: 1 MGTSPAPFLVAGCLLTGLSL.....IDMDDIGIDSSDLVEDSFL 1089

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5652	100.0	1089	5 AAU84300	Aau84300 Human end
2	5652	100.0	1089	6 ABG72449	Abg72449 Human pla
3	5652	100.0	1089	6 ABP96312	Abp96312 Human pla
4	5652	100.0	1089	7 ABR84718	Abrr84718 Human PDG
5	5652	100.0	1089	7 ADF45081	Adf45081 Human kin
6	5652	100.0	1089	7 ADF90896	Adf90896 Human hep
7	5652	100.0	1089	8 ADM69012	Adm69012 Human pla
8	5652	100.0	1089	8 ADQ17833	Adq17833 Human sof
9	5652	100.0	1089	8 ADQ59532	Adq59532 Human can
10	5652	100.0	1089	8 ADQ39641	Adq39641 Human myo
11	5649	99.9	1089	2 AAR06910	Aar06910 Alpha typ
12	5649	99.9	1089	6 ABG72453	Abg72453 Human pla
13	5648	99.9	1089	6 ABG72450	Abg72450 Human pla
14	5647	99.9	1089	6 ABG72452	Abg72452 Human pla
15	5646	99.9	1089	6 ABG72451	Abg72451 Human pla
16	5645	99.9	1089	2 AAR08267	Aar08267 Platelet
17	5645	99.9	1089	8 ADM69031	Adm69031 Human PDG
18	5643	99.8	1089	8 ADM69034	Adm69034 Human PDG
19	5640	99.8	1089	8 ADM69035	Adm69035 Human PDG
20	5637	99.7	1089	8 ADM69020	Adm69020 Human PDG
21	5636.5	99.7	1088	5 AAO17356	Aao17356 Human pla
22	5617.5	99.4	1084	8 ADM69033	Adm69033 Human PDG
23	5617	99.4	1085	8 ADM69016	Adm69016 Human PDG
24	5614.5	99.3	1086	8 ADM69018	Adm69018 Human PDG
25	5602.5	99.1	1084	8 ADM69022	Adm69022 Human PDG

26	5533	97.9	1089	8 ADM69037	Adm69037 Human PDG
27	5232	92.6	1096	8 ADQ59529	Adq59529 Human can
28	5154	91.2	1009	2 AAR26206	Aar26206 Type B hu
29	3046	53.9	589	6 ABG72454	Abg72454 Human pla
30	2693.5	47.7	834	8 ADJ93550	Adj93550 NM_030917
31	2692	47.6	849	8 ADJ93549	Adj93549 NM_030917
32	2676.5	47.4	811	8 ADJ93552	Adj93552 NM_030917
33	2676.5	47.4	826	8 ADJ93551	Adj93551 NM_030917
34	2359.5	41.7	1106	2 AAR26205	Aar26205 Type B hu
35	2354.5	41.7	1106	1 AAP90127	Aap90127 Platelet
36	2354.5	41.7	1106	2 AAR99690	Aar99690 Platelet
37	2354.5	41.7	1106	6 ABG72459	Abg72459 Human pla
38	2354.5	41.7	1106	6 ABP96311	Abp96311 Human pla
39	2354.5	41.7	1106	7 ABR84719	Abrr84719 Human PDG
40	2354.5	41.7	1106	7 ADF45082	Adf45082 Human kin
41	2354.5	41.7	1106	8 ABO84679	Abo84679 Human can
42	2351	41.6	1107	8 ABO84677	Abo84677 Human can
43	2350.5	41.6	1106	6 ABG72456	Abg72456 Human pla
44	2349.5	41.6	1106	6 ABG72458	Abg72458 Human pla
45	2348.5	41.6	1106	6 ABG72457	Abg72457 Human pla

ALIGNMENTS

RESULT 1  
AAU84300  
ID AAU84300 standard; protein; 1089 AA.  
XX  
AC AAU84300;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Human endometrial cancer related protein, PDGFRA.  
XX  
KW Human; endometrial cancer; differential expression; DNA microarray;  
KW protein microarray.  
XX  
OS Homo sapiens.  
XX  
PN WO200209573-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 31-JUL-2001; 2001WO-US024104.  
XX  
PR 31-JUL-2000; 2000US-0221735P.  
XX  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
XX  
PI Mutter GL;  
XX  
DR WPI; 2002-179967/23.  
DR N-PSDB; ABK35520.  
XX  
PT Diagnosing endometrial cancer comprises determining expression of nucleic acid molecules or expression products that are differentially expressed in normal and malignant endometrium.  
XX  
PS Claim 33; Page 214-217; 233pp; English.  
XX  
CC The invention relates to diagnosing endometrial cancer in a subject suspected of having endometrial cancer comprising determining the expression of a set of nucleic acid molecules or expression products in an endometrial sample suspected of being cancerous, where the set of nucleic acid molecules comprises at least 2 nucleic acid molecules selected from 50 fully defined sequences as given in the specification. The nucleic acids are used as an array of at least 2 of the 50 nucleic acids bound to a solid substrate. Also included is a solid-phase protein microarray comprising at least 2 antibodies or its antigen binding fragments, that specifically bind at least 2 different polypeptides from the 50 fully defined sequences as given in the specification, fixed to a solid substrate. The methods and arrays are useful for the diagnosis of

CC endometrial cancer, selecting and monitoring treatment regimes and  
CC identification of lead compounds useful for the treatment of endometrial  
CC cancer. The present sequence is one of 50 proteins differentially  
CC expressed between cancerous and non-cancerous samples  
XX  
SQ Sequence 1089 AA;  
Query Match 100.0%; Score 5652; DB 5; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGTSHPAFLVGLLGLTGLSLILCOLSLPLPNEKVKQLNSFSIRCFGESEVSWQYP 60  
DB 1 MGTSHPAFLVGLLGLTGLSLILCOLSLPLPNEKVKQLNSFSIRCFGESEVSWQYP 60  
QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELSGRIHIY 120  
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QY 121 VPDPAVAFPLGWTDLVIVVEDDSALIPCRITDPPTVTLHNSGVVPASYSROGFNG 180  
DB 121 VPDPAVAFPLGWTDLVIVVEDDSALIPCRITDPPTVTLHNSGVVPASYSROGFNG 180  
QY 181 TPTVGPVCEATVKGKFKQIPENVYALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
DB 181 TPTVGPVCEATVKGKFKQIPENVYALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
QY 241 EVVDLQWYTGVEKVGKIGITMLEIKVPSIKLVTLTVPEATVXDSGDYECARQATREV 300  
DB 241 EVVDLQWYTGVEKVGKIGITMLEIKVPSIKLVTLTVPEATVXDSGDYECARQATREV 300  
QY 301 EMKVTISVHEKGFIEIKPTFSOLEAVNLHVEHFVVEVRAYPPRISMLKNLTLIENL 360  
DB 301 EMKVTISVHEKGFIEIKPTFSOLEAVNLHVEHFVVEVRAYPPRISMLKNLTLIENL 360  
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DB 361 TEITTDVEKIQEIRYRSKLIIRAKEDSGHYITVAQNEADAVKSYTFELLTQVPSILD 420  
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DB 421 VDDHSGTGQVRCVTAEGTPELDIEWMICKDITKCNNETSWTLANNYSNIITEHSRD 480  
QY 481 RSTVEGRVTPAKVEETIAVRLAKNLGAENRELKLVAPTIRSELTVAAAVLLVIVII 540  
DB 481 RSTVEGRVTPAKVEETIAVRLAKNLGAENRELKLVAPTIRSELTVAAAVLLVIVII 540  
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DB 601 SGAFGKVVETAYGLRSQPMKAVKMLKPTARSSEKQALMSLXIMTHLGPLHIVNL 660  
QY 661 LGACTKSGPIYIITEYCFYGDVLYNLHKNRDSFLSHHPKPKKELDIFGLNPADESTRSY 720  
DB 661 LGACTKSGPIYIITEYCFYGDVLYNLHKNRDSFLSHHPKPKKELDIFGLNPADESTRSY 720  
QY 721 VILSPENNGDYMOKQADTTQYVPMLEKRVESKYSDIQRSLYDRPASYSKKKSMLDSEVK 780  
DB 721 VILSPENNGDYMOKQADTTQYVPMLEKRVESKYSDIQRSLYDRPASYSKKKSMLDSEVK 780  
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DB 781 LLSDDNSGUTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840  
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DB 841 RDIHDSNYVSKGSTFLPVKWMAPESIFDNLTYTLLSDVMSYIGILLWEIFSLGGTYPGMM 900  
QY 901 VDSFTFNKIKSGYRMKAPDHATSEVYIEMVKWNSPEKRPSPYHLSEIVENLLPGQYKK 960  
DB 901 VDSFTFNKIKSGYRMKAPDHATSEVYIEMVKWNSPEKRPSPYHLSEIVENLLPGQYKK 960

DB 901 VDSFTFNKIKSGYRMKAPDHATSEVYIEMVKWNSPEKRPSPYHLSEIVENLLPGQYKK 960  
QY 961 SYEKIHLDFLKSDHPAVARMVDSNAYIGVTYKNEEDKLKOWEGGLDEORLSADSGYII 1020  
DB 961 SYEKIHLDFLKSDHPAVARMVDSNAYIGVTYKNEEDKLKOWEGGLDEORLSADSGYII 1020  
QY 1021 PLPDDIPVPEEEDLGRNRHSSQTSSESAIETGSSSTPIKREDETIEDIMMDDIGIDS 1080  
DB 1021 PLPDDIPVPEEEDLGRNRHSSQTSSESAIETGSSSTPIKREDETIEDIMMDDIGIDS 1080  
QY 1081 SLDVEDSFL 1089  
DB 1081 SLDVEDSFL 1089  
RESULT 2  
ABG72449  
ID ABG72449 standard; protein; 1089 AA.  
XX  
AC ABG72449;  
XX  
DT 13-FEB-2003 (first entry)  
XX  
Human platelet derived growth factor receptor alpha.  
DE  
XX  
Human; platelet derived growth factor receptor alpha; PDGFRalpha;  
KW hepatocytic; dermatological; nephrotropic; vulnary; ophthalmological;  
KW cytosolic; gene therapy; vaccine; phosphoinositide-kinase-inhibitor-3;  
KW phospholipase-inhibitor-C; receptor tyrosine kinase; cell proliferation;  
KW cell migration; extracellular matrix synthesis; secretion;  
KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;  
KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;  
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy.  
XX  
Homo sapiens.  
OS  
XX  
Key Location/Qualifiers  
FH Domain 1..490  
FT /label= Extracellular\_domain  
FT Peptide 1..24  
FT /label= Signal\_peptide\_sequence\_2  
FT Peptide 1..20  
FT /label= Signal\_peptide\_sequence\_1  
FT Protein 21  
FT /label= Mature\_PDGR\_sequence\_1  
FT Protein 25  
FT /label= Mature\_PDGR\_sequence\_2  
FT Domain 42..102  
FT /label= Immunoglobulin-like\_domain  
FT Domain 143..191  
FT /label= Immunoglobulin-like\_domain  
FT Domain 228..292  
FT /label= Immunoglobulin-like\_domain  
FT Domain 338..399  
FT /label= Immunoglobulin-like\_domain  
FT /note= "6"  
FT Domain 428..503  
FT /label= Immunoglobulin-like\_domain  
FT Domain 535..548  
FT /label= Transmembrane\_domain  
FT Domain 549..1055  
FT /label= Intracellular\_domain  
FT Domain 556..661  
FT /note= "Split tyrosine kinase domain segment 1"  
FT Domain 760..900  
FT /note= "Split tyrosine kinase domain segment 2"  
XX  
US2002111304-A1.  
PN  
XX  
15-AUG-2002.  
XX  
25-MAY-2001; 2001US-00866510.  
XX





XX	CC	The present invention relates to a method of treating a vascular condition in a mammal, which comprises administering to the mammal a therapeutic amount of endothelial precursor cells. The method and cells of the invention are useful for treating a vascular condition, e.g. myocardial infarction, atherosclerosis, ischaemia, tachycardia, congestive heart failure, peripheral vasculature disorder, hypertension, stroke, thrombosis, arrhythmia or tachycardia. The present sequence is a protein shown in the exemplification of the invention
XX	CC	Sequence 1089 AA;
XX	CC	Query Match 100.0%; Score 5652; DB 7; Length 1089;
XX	CC	Best Local Similarity 100.0%; Pred. No. 0;
XX	CC	Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60
DB	1	MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60
QY	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYIY 120
DB	61	MSEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYIY 120
QY	121	VDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVWPASYSRQGFNG 180
DB	121	VDPDVAFVPLGMDTYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVWPASYSRQGFNG 180
QY	181	TFTVGPYICVATVKGKFKQIIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240
DB	181	TFTVGPYICVATVKGKFKQIIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240
QY	241	EVVDLQWTVGEGVKGIGITLMBEIKVPSIKLVTVLTPVATVKGSDGYECARQAQREV 300
DB	241	EVVDLQWTVGEGVKGIGITLMBEIKVPSIKLVTVLTPVATVKGSDGYECARQAQREV 300
QY	301	EMKKVTISVHEKGFBIKPTFSQLEAVNLHVEVKHFVVEVRAVPPPRISMLKNLTLIENL 360
DB	301	EMKKVTISVHEKGFBIKPTFSQLEAVNLHVEVKHFVVEVRAVPPPRISMLKNLTLIENL 360
QY	361	TEITTOVEKIQIRYRSKLIIRAKEEDSGHYITVAQNEADVKSYPFELLTQVPSSILD 420
DB	361	TEITTOVEKIQIRYRSKLIIRAKEEDSGHYITVAQNEADVKSYPFELLTQVPSSILD 420
QY	421	VDDHGSCTGQVRCVTAEGTPLDIEWMICKDICKCNNTSWTILANNYSNIITEIHSRD 480
DB	421	VDDHGSCTGQVRCVTAEGTPLDIEWMICKDICKCNNTSWTILANNYSNIITEIHSRD 480
QY	481	RSTVEGRVTFKVEETIAVRCLAKNLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540
DB	481	RSTVEGRVTFKVEETIAVRCLAKNLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540
QY	541	SLILVVIWKKQPRYIRWRVIESIPDGHEIYIYDPMQLPYDSRWEFFRDLGLVGRVLG 600
DB	541	SLILVVIWKKQPRYIRWRVIESIPDGHEIYIYDPMQLPYDSRWEFFRDLGLVGRVLG 600
QY	601	SGAFKGVVETAGLRSQPMKAVKMLKPTARSSEKQALMSLKMTHLGLPHLIVNL 660
DB	601	SGAFKGVVETAGLRSQPMKAVKMLKPTARSSEKQALMSLKMTHLGLPHLIVNL 660
QY	661	LGACTKSGPIIITTEYCFYGDVLYLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720
DB	661	LGACTKSGPIIITTEYCFYGDVLYLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720
QY	721	VILSPFNNGDYMOKQADTTQVPMLEKEVSKYSDIQRSLYDRPASYKKSKMLDSEVK 780
DB	721	VILSPFNNGDYMOKQADTTQVPMLEKEVSKYSDIQRSLYDRPASYKKSKMLDSEVK 780
QY	781	LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLAQGIKVICDFGLA 840
DB	781	LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLAQGIKVICDFGLA 840
QY	841	RDIMHDSNTVSKGSTPLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900

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Db      1  MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSILRCFGESEVSWQYP 60
QY      61  MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120
Db      61  MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120
QY      121  VPDPDAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASVDSROGFGNG 180
Db      121  VPDPDAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASVDSROGFGNG 180
QY      181  TPTVGPYICBATVKGKGFQTIIPNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
Db      181  TPTVGPYICBATVKGKGFQTIIPNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
QY      241  EYVDLQWTPYGEVKGKGIITMLEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
Db      241  EYVDLQWTPYGEVKGKGIITMLEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
QY      301  EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVHFVVEVRAVPPRISMLKNNLTLENL 360
Db      301  EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVHFVVEVRAVPPRISMLKNNLTLENL 360
QY      361  TEITDVEKIQEIYRSKLIIRAKEEDSGHYITVAQNEDAVKSYTFELLTQVPSIIDL 420
Db      361  TEITDVEKIQEIYRSKLIIRAKEEDSGHYITVAQNEDAVKSYTFELLTQVPSIIDL 420
QY      421  VDDHSGTGQVRCRTAEGTLPDIEWMICKDKIKCNETSWITLANNVSNITTEIHSRD 480
Db      421  VDDHSGTGQVRCRTAEGTLPDIEWMICKDKIKCNETSWITLANNVSNITTEIHSRD 480
QY      481  RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540
Db      481  RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540
QY      541  SLIVLVVIMKQKPRYRIRMRVIESIPDGHETIYVDPMLQPSYDRWEFFPRDGLVLRGLG 600
Db      541  SLIVLVVIMKQKPRYRIRMRVIESIPDGHETIYVDPMLQPSYDRWEFFPRDGLVLRGLG 600
QY      601  SGAFKGVETATGLRSQPMKAVKMLPTARSSEKQALMSELKIMHGLPHINIVNL 660
Db      601  SGAFKGVETATGLRSQPMKAVKMLPTARSSEKQALMSELKIMHGLPHINIVNL 660
QY      661  LGACTKSGPIYIITEYCFYGDVLYNLHKNRDSFLSHPEKPKKELDI FGLNPADESTRSY 720
Db      661  LGACTKSGPIYIITEYCFYGDVLYNLHKNRDSFLSHPEKPKKELDI FGLNPADESTRSY 720
QY      721  VILSFENNGDYMCKQADTTQYVPMLEKEVSKYDIQSLYDRPASYYKKSMLDSEVKX 780
Db      721  VILSFENNGDYMCKQADTTQYVPMLEKEVSKYDIQSLYDRPASYYKKSMLDSEVKX 780
QY      781  LLSDDNSEGITLIDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840
Db      781  LLSDDNSEGITLIDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840
QY      841  RDIIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSGVMSYGLLWEISLGTTPYGMW 900
Db      841  RDIIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSGVMSYGLLWEISLGTTPYGMW 900
QY      901  VDSFTYNNKISGYRMAKPDHATSEVYEIMVKCNSEPEKRPSPYHISEIVENLLPGQYKK 960
Db      901  VDSFTYNNKISGYRMAKPDHATSEVYEIMVKCNSEPEKRPSPYHISEIVENLLPGQYKK 960
QY      961  SYEKIHLDFLKSHPAVARNRVDSDNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII 1020
Db      961  SYEKIHLDFLKSHPAVARNRVDSDNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII 1020
QY      1021  PLPDIDPVEEDLGRNHRSSQTSSESALETGSSSTFKRDETIEDIDMDDDIGIDS 1080
Db      1021  PLPDIDPVEEDLGRNHRSSQTSSESALETGSSSTFKRDETIEDIDMDDDIGIDS 1080
QY      1081  SLDVDSFL 1089

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Db      1081  SLDVDSFL 1089
RESULT 6
ID      ADF90896
XX      ADF90896 standard; protein; 1089 AA.
XX      ADF90896;
XX      AC
XX      26-FEB-2004 (first entry)
XX      Human hepatic-fibrosis disease marker protein SEQ ID 358.
DE      Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;
XX      hepatic carcinoma; human.
XX      Homo sapiens.
OS      XX
PN      JP2003259877-A.
PD      16-SEP-2003.
XX      PF 11-MAR-2002; 2002JP-00065013.
XX      PR 11-MAR-2002; 2002JP-00065013.
XX      (SUMU ) SUMITOMO SEIYAKU KK.
XX      WPI; 2003-821598/77.
DR      XX
XX      Hepatic fibrosis disease markers comprising polynucleotides or
PT      antibodies, useful for improved diagnosis, screening and developing drugs
PT      to treat hepatitis, to control cirrhosis and carcinoma.
XX      PS Claim 3; SEQ ID NO 358; 313pp; Japanese.
XX      CC The present invention relates to hepatic-fibrosis disease markers
CC      (ADF90539-ADF90871) and related proteins (ADF90872-ADF90917). The
CC      sequences are useful for detecting and treating hepatic fibrosis caused
CC      by alcohol consumption, virus infection, etc., and the associated chronic
CC      hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The
CC      markers allow the cause of hepatic fibrosis to be clarified (diagnostic
CC      precision), so more suitable treatments can be developed and given.
XX      SQ Sequence 1089 AA;
Query Match 100.0%; Score 5652; DB 7; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSILRCFGESEVSWQYP 60
Db      1  MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSILRCFGESEVSWQYP 60
QY      61  MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120
Db      61  MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120
QY      121  VPDPDAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASVDSROGFGNG 180
Db      121  VPDPDAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASVDSROGFGNG 180
QY      181  TPTVGPYICBATVKGKGFQTIIPNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
Db      181  TPTVGPYICBATVKGKGFQTIIPNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240
QY      241  EYVDLQWTPYGEVKGKGIITMLEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
Db      241  EYVDLQWTPYGEVKGKGIITMLEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
QY      301  EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVHFVVEVRAVPPRISMLKNNLTLENL 360
Db      301  EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVHFVVEVRAVPPRISMLKNNLTLENL 360

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QY 361 TEITDVEKIQRYSKLIIRAKBEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420
Db 361 TEITDVEKIQRYSKLIIRAKBEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420
QY 421 VDDHSGTGQVRCRTAEGTLPDIEWMICKDKKCNNETSWILANNVSNIIIEHSRD 480
Db 421 VDDHSGTGQVRCRTAEGTLPDIEWMICKDKKCNNETSWILANNVSNIIIEHSRD 480
QY 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVII 540
Db 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVII 540
QY 541 SLIVLVVWVKQPRYRIRWRVIESISPDGHEIYVDPMLPYDSRWEFFRDGLVLRVLG 600
Db 541 SLIVLVVWVKQPRYRIRWRVIESISPDGHEIYVDPMLPYDSRWEFFRDGLVLRVLG 600
QY 601 SGAFKGVVEGTAYGLRSQPMKAVAKMLKPTARSSEKQALMSELKIMTHLGHPLINVL 660
Db 601 SGAFKGVVEGTAYGLRSQPMKAVAKMLKPTARSSEKQALMSELKIMTHLGHPLINVL 660
QY 661 LGACTKSGPIYIITEYCFYGDVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIYIITEYCFYGDVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
QY 721 VILSFENNGDYMOMKQADTTQYVPMLEKEVSKYSIDQRSLYDRPASYYKKKSMLDSEVK 780
Db 721 VILSFENNGDYMOMKQADTTQYVPMLEKEVSKYSIDQRSLYDRPASYYKKKSMLDSEVK 780
QY 781 LLSDDNSEGLTLLDLSFTYQVARGHEFLASKNCVHRDLAARNVLLAOGKIVIKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLSFTYQVARGHEFLASKNCVHRDLAARNVLLAOGKIVIKICDFGLA 840
QY 841 RDIHDSNVYKSGSTFLPVKWMAPESIFDNLTYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900
Db 841 RDIHDSNVYKSGSTFLPVKWMAPESIFDNLTYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900
QY 901 VDSFTFYNKIKSGYMAKPDHATSEVYIEMVKCNWSEPEKPSFYHLSEIVENLLPQYKK 960
Db 901 VDSFTFYNKIKSGYMAKPDHATSEVYIEMVKCNWSEPEKPSFYHLSEIVENLLPQYKK 960
QY 961 SYEKIHLDFLKSHPAVARNRVDSDNAYIGVTYKNEEDKLDWEGGLDEORLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARNRVDSDNAYIGVTYKNEEDKLDWEGGLDEORLSADSGYII 1020
QY 1021 PLPDIDPVPEEDLGRNHRSSQTSSESATETGSSSTFIKREDETIEDIDMDDIGIDS 1080
Db 1021 PLPDIDPVPEEDLGRNHRSSQTSSESATETGSSSTFIKREDETIEDIDMDDIGIDS 1080
QY 1081 SLDVEDSFL 1089
Db 1081 SLDVEDSFL 1089
RESULT 7
ADM69012
ID ADM69012 standard; protein; 1089 AA.
XX
AC ADM69012;
XX
AC ADM69012;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human platelet derived growth factor receptor alpha wild-type protein.
XX
KW platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW type III receptor tyrosine kinase; RTK; enzyme; receptor; wild-type.
XX
OS Homo sapiens.
XX
PN WO2003105773-A2.
XX
PD 24-DEC-2003.
XX
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PF 13-JUN-2003; 2003WO-US018901.
XX
PR 13-JUN-2002; 2002US-0389107P.
PR 08-JAN-2003; 2003US-0438999P.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (DAND ) DANA FARBEN CANCER INST INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI Heinrich MC, Corless CL, Fletcher JA, Demetri GD;
XX
XX WPI; 2004-082052/08.
DR N-PSDB; ADM69011, ADM69029.
XX
XX New isolated variant platelet derived growth factor alpha (PDGFRA)
PT polypeptide, useful for screening for a compound useful in influencing
PT PDGFRA-mediated neoplasia in a mammal.
XX
XX Example 1; SEQ ID NO 2; 302pp; English.
XX
CC The invention relates to a novel isolated variant platelet derived growth
CC factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC for screening for a compound that may influence PDGFRA-mediated neoplasia
CC in a mammal. The current sequence is that of the human PDGFRA wild-type
CC protein of the invention.
XX
XX Sequence 1089 AA;
QY Query Match 100.0%; Score 5652; DB 8; Length 1089;
Db Best Local Similarity 100.0%; Pred. No. 0;
QY Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MGTSHPAFLVGLGCLLTGLSLILCOLSLPSTLPNENKVVQLNSSFSLRCFGESEVSWQYP 60
QY 1 MGTSHPAFLVGLGCLLTGLSLILCOLSLPSTLPNENKVVQLNSSFSLRCFGESEVSWQYP 60
Db 61 MSEESESDVEIRNEENNSGLFVTLEVSASSAAHTGLTYCYNHTQTETNELEGRHIYIY 120
QY 61 MSEESESDVEIRNEENNSGLFVTLEVSASSAAHTGLTYCYNHTQTETNELEGRHIYIY 120
Db 61 MSEESESDVEIRNEENNSGLFVTLEVSASSAAHTGLTYCYNHTQTETNELEGRHIYIY 120
QY 121 VPDPPVAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASYSRQGFNG 180
Db 121 VPDPPVAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASYSRQGFNG 180
QY 181 TFTVGPYICBATVKGKFFOTIPFNVALKATSELDLEMEALKTVYKSGETIIVTCAVFN 240
Db 181 TFTVGPYICBATVKGKFFOTIPFNVALKATSELDLEMEALKTVYKSGETIIVTCAVFN 240
QY 241 EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
Db 241 EVVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREV 300
QY 301 EMKKTIVISHEKGFIEIKPTFSQLEAVNLHEVGHFVVEVRAVPPPRISWLKNLTLIENL 360
Db 301 EMKKTIVISHEKGFIEIKPTFSQLEAVNLHEVGHFVVEVRAVPPPRISWLKNLTLIENL 360
QY 361 TEITDVEKIQRYSKLIIRAKBEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420
Db 361 TEITDVEKIQRYSKLIIRAKBEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420
QY 421 VDDHSGTGQVRCRTAEGTLPDIEWMICKDKKCNNETSWILANNVSNIIIEHSRD 480
Db 421 VDDHSGTGQVRCRTAEGTLPDIEWMICKDKKCNNETSWILANNVSNIIIEHSRD 480
QY 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVII 540
Db 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVII 540
QY 541 SLIVLVVWVKQPRYRIRWRVIESISPDGHEIYVDPMLPYDSRWEFFRDGLVLRVLG 600
Db 541 SLIVLVVWVKQPRYRIRWRVIESISPDGHEIYVDPMLPYDSRWEFFRDGLVLRVLG 600
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QY 601 SGAFKVEGTAYCLSRQPMKAVKMLKPTARSEKQALMSKELKIMTHLGHNLIVNL 660  
 DB 601 SGAFKVEGTAYCLSRQPMKAVKMLKPTARSEKQALMSKELKIMTHLGHNLIVNL 660  
 QY 661 LGACTKSGPIIITEYCFYGLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720  
 DB 661 LGACTKSGPIIITEYCFYGLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720  
 QY 721 VILSFENNGYMDMKQADTTQYVPMLEKVEKYSYDIQSLYDRPASYSKKKMLDSEVKV 780  
 DB 721 VILSFENNGYMDMKQADTTQYVPMLEKVEKYSYDIQSLYDRPASYSKKKMLDSEVKV 780  
 QY 781 LLSDDNSEGLTLDDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840  
 DB 781 LLSDDNSEGLTLDDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840  
 QY 841 RDMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGTPYPGMM 900  
 DB 841 RDMHDSNYVSKGSTFLPVKWMAPESIFDNLTYTTLSDVWSYGILLWEIFSLGTPYPGMM 900  
 QY 901 VDSIFYNKISGRMAKPDHATSEVYBIMVKWNSPEKRPSPYHLSIIVENLLPGQYKK 960  
 DB 901 VDSIFYNKISGRMAKPDHATSEVYBIMVKWNSPEKRPSPYHLSIIVENLLPGQYKK 960  
 QY 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVYKNEEDKLDWEGGLDEORLSADSGYII 1020  
 DB 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVYKNEEDKLDWEGGLDEORLSADSGYII 1020  
 QY 1021 PLPDIDPVEEDLGRNHRSSQTSESAIETGSSSTFIKREDETIEDIMDDIGIDS 1080  
 DB 1021 PLPDIDPVEEDLGRNHRSSQTSESAIETGSSSTFIKREDETIEDIMDDIGIDS 1080  
 QY 1081 SLDVDSFL 1089  
 DB 1081 SLDVDSFL 1089

RESULT 8  
 ADQ17833  
 ID ADQ17833 standard; protein; 1089 AA.  
 AC ADQ17833;  
 XX ADQ17833;  
 DT 26-AUG-2004 (first entry)  
 XX Human soft tissue sarcoma-upregulated protein - SEQ ID 650.  
 DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.  
 KW Homo sapiens.  
 XX Homo sapiens.  
 XX WO2004048938-A2.  
 XX 10-JUN-2004.  
 XX 26-NOV-2003; 2003WO-US038193.  
 XX 26-NOV-2002; 2002US-0429739P.  
 XX (PROT-) PROTEIN DESIGN LABS INC.  
 XX Aziz N, Ginsburg WM, Zlotnik A;  
 XX WPI; 2004-441208/41.  
 XX Early detection of soft tissue sarcoma comprises determining expression  
 PT of a gene in a first soft tissue sample and a normal soft tissue sample  
 PT and comparing the gene expression, also useful in treating soft tissue  
 PT sarcoma.  
 XX Example 2; SEQ ID NO 650; 210pp; English.

CC The invention relates to a novel method for detecting soft tissue sarcoma  
 CC which comprises obtaining a first soft tissue sample from an individual  
 CC and a normal soft tissue sample from the same or different individual,  
 CC determining the expression of a gene in both samples and comparing the  
 CC expression of the gene in both soft tissue samples, where a higher level  
 CC of protein expression in the first soft tissue sample indicates the  
 CC presence of soft tissue sarcoma. The method of the invention has  
 CC cytotatic applications and may be useful for detecting soft tissue  
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
 CC acid sequences may be useful in diagnostic and screening applications.  
 CC The current sequence is that of a human soft tissue sarcoma-upregulated  
 CC protein of the invention. The current sequence is not shown within the  
 CC specification per se but was submitted in CD format by the inventor.  
 XX Sequence 1089 AA;  
 SQ

Query Match 100.0%; Score 5652; DB 8; Length 1089;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches: 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQVP 60  
 DB 1 MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQVP 60  
 QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120  
 DB 61 MSEEESDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120  
 QY 121 VPDPAVAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASVDSRQGFNG 180  
 DB 121 VPDPAVAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASVDSRQGFNG 180  
 QY 181 TPTVGYICEATVKGKFKOTIPFNVALKATSELDLEMEALKTVYKSGTIVVTCVFN 240  
 DB 181 TPTVGYICEATVKGKFKOTIPFNVALKATSELDLEMEALKTVYKSGTIVVTCVFN 240  
 QY 241 EVVDLQWTPYGEVKGKGIITMLEBEIKVPSIKLVYTLTVPEATVKDSDGYECAAQATREV 300  
 DB 241 EVVDLQWTPYGEVKGKGIITMLEBEIKVPSIKLVYTLTVPEATVKDSDGYECAAQATREV 300  
 QY 301 EMKKTIVSVHEKGFIBIKPTFSQLEAVNLHVKHFVVEVRAVPPPPRISLKNLTLIENL 360  
 DB 301 EMKKTIVSVHEKGFIBIKPTFSQLEAVNLHVKHFVVEVRAVPPPPRISLKNLTLIENL 360  
 QY 361 TEITDVEKIQEIRVRSKULIRAKEEDSGHYTIVAAQNEADAVKSYTFELLTQVPSIIDL 420  
 DB 361 TEITDVEKIQEIRVRSKULIRAKEEDSGHYTIVAAQNEADAVKSYTFELLTQVPSIIDL 420  
 QY 421 VDDHGSTGGQVRCVTAECTPLPDIEWMICKDIKKCNNTSWTILANNVSNITIEHSRD 480  
 DB 421 VDDHGSTGGQVRCVTAECTPLPDIEWMICKDIKKCNNTSWTILANNVSNITIEHSRD 480  
 QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLSRSELTVAANLVLLVIVII 540  
 DB 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLSRSELTVAANLVLLVIVII 540  
 QY 541 SLILVLIWIKQKPRVIRWRVIESIPDGHEVYIVDPMOLPYDSRWEFFRDLGLVLRVLG 600  
 DB 541 SLILVLIWIKQKPRVIRWRVIESIPDGHEVYIVDPMOLPYDSRWEFFRDLGLVLRVLG 600  
 QY 601 SGAFKVEGTAYGLSRQPMKAVKMLKPTARSEKQALMSKELKIMTHLGHNLIVNL 660  
 DB 601 SGAFKVEGTAYGLSRQPMKAVKMLKPTARSEKQALMSKELKIMTHLGHNLIVNL 660  
 QY 661 LGACTKSGPIIITEYCFYGLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720  
 DB 661 LGACTKSGPIIITEYCFYGLVNLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720  
 QY 721 VILSFENNGYMDMKQADTTQYVPMLEKVEKYSYDIQSLYDRPASYSKKKMLDSEVKV 780  
 DB 721 VILSFENNGYMDMKQADTTQYVPMLEKVEKYSYDIQSLYDRPASYSKKKMLDSEVKV 780  
 QY 781 LLSDDNSEGLTLDDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840



Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQKIVKICDFGLA 840  
Qy 841 RDIMDSNVVSGSTFLPVKWWAPESIFDNLYTTLSDVMSYGILLWEIFSLGTPVPGNM 900  
Db 841 RDIMDSNVVSGSTFLPVKWWAPESIFDNLYTTLSDVMSYGILLWEIFSLGTPVPGNM 900  
Qy 901 VDSFTFNKIKSGYRMKPDHATSEVVEIMVKWNSPEKRPSPFYHLSEIVENLLPQYKK 960  
Db 901 VDSFTFNKIKSGYRMKPDHATSEVVEIMVKWNSPEKRPSPFYHLSEIVENLLPQYKK 960  
Qy 961 SYEKIHLDFKSDHPAVARMVDSDNAYIGVYKNEDKLDKWEGLDQRLSADSGYII 1020  
Db 961 SYEKIHLDFKSDHPAVARMVDSDNAYIGVYKNEDKLDKWEGLDQRLSADSGYII 1020  
Qy 1021 PLPDDIPVPEEDLGRNRHSSQTSSESATETGSSSTFIKREDETIEDIDMDDIGIDS 1080  
Db 1021 PLPDDIPVPEEDLGRNRHSSQTSSESATETGSSSTFIKREDETIEDIDMDDIGIDS 1080  
Qy 1081 SDLVEDSFL 1089  
Db 1081 SDLVEDSFL 1089

RESULT 9  
ADQ59532 standard; protein; 1089 AA.  
XX ADQ59532;  
XX ADQ59532;  
DT 07-OCT-2004 (first entry)  
XX Human cancer-associated (CA) protein sequence SEQ ID NO:168.  
DE human; cancer-associated gene; cancer-associated protein; cytostatic;  
XX human; cancer-associated gene; cancer-associated protein; cytostatic;  
KW gene therapy; vaccine; tyrosine kinase antagonist;  
KW G-protein coupled receptor antagonist; cancer; lymphoma.  
XX Homo sapiens.  
XX WO2004058288-A1.  
PN 15-JUL-2004.  
XX 15-DEC-2003; 2003WO-US040082.  
PF 17-DEC-2002; 2002US-00322696.  
PR (SAGR-) SAGRES DISCOVERY INC.  
XX Morris DW, Malandro MS;  
PI WPI; 2004-543349/52.  
XX N-PSDB; ADQ59530, ADQ59531.  
DR New cancer-associated nucleic acid for diagnosing, preventing or treating  
PT cancer (e.g. lymphoma) or for screening agents that may be used for  
PT treating or preventing cancer.  
XX Claim 19; SEQ ID NO 168; 143pp; English.  
PS The present invention describes human cancer-associated (CA) nucleotide  
CC sequences (I). Also described: (1) an expression vector comprising (I);  
CC (2) a host cell comprising (I) or the expression vector; (3) a microarray  
CC for detecting a CA nucleic acid; (4) an isolated polypeptide encoded  
CC within an open reading frame of a CA sequence; (5) an isolated antibody,  
CC or its antigen binding fragment, that binds to the above polypeptide; (6)  
CC a hybridoma that produces the monoclonal antibody described above; (7) a  
CC pharmaceutical composition comprising the antibody and a pharmaceutical  
CC excipient; (8) a kit for detecting or diagnosing cancer cells, comprising  
CC the above (monoclonal) antibody or polynucleotide that selectively  
CC hybridizes to any of the polynucleotide sequences mentioned above; (9)  
CC methods for diagnosing cancer or for detecting the presence or absence of

CC cancer cells in an individual; (10) a method for inhibiting growth of  
CC cancer cells in an individual; (11) a method for delivering a therapeutic  
CC agent to cancer cells in an individual; (12) an electronic library  
CC comprising the polynucleotide or polypeptide, or their fragments,  
CC mentioned above; (13) a method of screening for anticancer activity; (14)  
CC methods for detecting cancer associated with expression of a polypeptide  
CC or the presence of the antibody in a test cell or serum sample; (15) a  
CC method for screening for a bioactive agent capable of modulating the  
CC activity of a CA protein encoded by the above nucleic acid molecule; and  
CC (16) a method for treating cancers. (I) has cytostatic activity, and can  
CC be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,  
CC and as a G-protein coupled receptor antagonist. The compositions and  
CC methods of the present invention can be used for diagnosing, preventing  
CC and treating cancer, especially lymphomas. They may also be used in  
CC screening for agents that may be used for treating or preventing cancer.  
CC The present sequence represents a human CA gene amino acid sequence,  
CC which is given in the exemplification of the present invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 1089 AA;  
Qy Query Match 100.0%; Score 5652; DB 8; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGTSHPAFLVGLCLTGLSLILCOLSLPSILPNEKVVQLNSSFRLRCFGESEVSWQYP 60  
Db 1 MGTSHPAFLVGLCLTGLSLILCOLSLPSILPNEKVVQLNSSFRLRCFGESEVSWQYP 60  
Qy 61 MSEEESDSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNNHTQTEENLEGRHIYY 120  
Db 61 MSEEESDSDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNNHTQTEENLEGRHIYY 120  
Qy 121 VPDPOVAFVPLGMDYLVIVEDDDSAIIPCRTTDPPTVTLNSEGVPASYSRQGFNG 180  
Db 121 VPDPOVAFVPLGMDYLVIVEDDDSAIIPCRTTDPPTVTLNSEGVPASYSRQGFNG 180  
Qy 181 TETVGPYICEATVKGKGFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
Db 181 TETVGPYICEATVKGKGFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
Qy 241 EVVDLQWTPYGEVKGKGIITMBEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300  
Db 241 EVVDLQWTPYGEVKGKGIITMBEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300  
Qy 301 EMKQVTISVHEKGFIEIKPTFSQLEAVNLHEVKGHFVVEVRAYPPPRISMLKNNLTLEN 360  
Db 301 EMKQVTISVHEKGFIEIKPTFSQLEAVNLHEVKGHFVVEVRAYPPPRISMLKNNLTLEN 360  
Qy 361 TEITTDVEKIQEIRYRSKULIRAKEEDSGHYTIVAQNEADAVKSYTFELLTQVPSILDL 420  
Db 361 TEITTDVEKIQEIRYRSKULIRAKEEDSGHYTIVAQNEADAVKSYTFELLTQVPSILDL 420  
Qy 421 VDDHGGSTGGQVRCCTAECTPLPDIEWMICKDKKCNNETSWTILANNVSNITIEHSRD 480  
Db 421 VDDHGGSTGGQVRCCTAECTPLPDIEWMICKDKKCNNETSWTILANNVSNITIEHSRD 480  
Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540  
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540  
Qy 541 SLILVLIWIKQPRYRWRVIESIPDGHXYIYDPMOLPYDSRWEFFRDGLVGRVLG 600  
Db 541 SLILVLIWIKQPRYRWRVIESIPDGHXYIYDPMOLPYDSRWEFFRDGLVGRVLG 600  
Qy 601 SGAFKVGVTGATYGLSRSPQVMKVAVKMLKPTARSSEKQALMSELKIMTHGLPHLIVNL 660  
Db 601 SGAFKVGVTGATYGLSRSPQVMKVAVKMLKPTARSSEKQALMSELKIMTHGLPHLIVNL 660  
Qy 661 LGACTKSGPIYITEYCFYGDVLVNLHKNRDSFLSHHPKPKKELDI FGLNPADESTRSY 720  
Db 661 LGACTKSGPIYITEYCFYGDVLVNLHKNRDSFLSHHPKPKKELDI FGLNPADESTRSY 720

Db 661 LGACTKSGPIIITTEYFCYGDVLYNLHKNRDSFLSHHPKPKKELDI FGLNPADESTRSY 720  
 QY 721 VILSFENNGDYMCKQADTTQYVPMLEKEVSKYDIQSLYDRPASYKKSMLESEVKN 780  
 Db 721 VILSFENNGDYMCKQADTTQYVPMLEKEVSKYDIQSLYDRPASYKKSMLESEVKN 780  
 QY 781 LLSDDNSEGLTLLDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
 Db 781 LLSDDNSEGLTLLDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
 QY 841 RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMW 900  
 Db 841 RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMW 900  
 QY 901 VDSFTFNKIKSGYRMKAPDHATSEVVEIMVKWNSPEKRPSPFYHLSEIVENLLPQYKK 960  
 Db 901 VDSFTFNKIKSGYRMKAPDHATSEVVEIMVKWNSPEKRPSPFYHLSEIVENLLPQYKK 960  
 QY 961 SYEKIHLDFLKSHPAVARVDSNAYIGVTKNEEDKLKDWEGGLDEORLSADSGYII 1020  
 Db 961 SYEKIHLDFLKSHPAVARVDSNAYIGVTKNEEDKLKDWEGGLDEORLSADSGYII 1020  
 QY 1021 PLPDIDPVEEDLGRNRHSSQTSESAIETGSSSTFIKREDETIEDIMMDDIGIDS 1080  
 Db 1021 PLPDIDPVEEDLGRNRHSSQTSESAIETGSSSTFIKREDETIEDIMMDDIGIDS 1080  
 QY 1081 SDLVEDSFL 1089  
 Db 1081 SDLVEDSFL 1089

RESULT 10  
 ADQ39641  
 ID ADQ39641 standard; protein; 1089 AA.  
 XX ADQ39641;  
 AC AC  
 XX AC  
 DT 18-NOV-2004 (first entry)  
 XX Human myocardial infarction-associated gene derived protein, SEQ ID 1304.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1304.  
 XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;  
 KW cardiant; gene therapy; human.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO2004058052-A2.  
 PN 15-JUL-2004.  
 PD 22-DEC-2003; 2003WO-US040978.  
 PP 20-DEC-2002; 2002US-0434778P.  
 PR 10-MAR-2003; 2003US-0453135P.  
 PR 30-APR-2003; 2003US-0466412P.  
 PR 23-SEP-2003; 2003US-0504955P.  
 XX (APPL-) APPLERA CORP.  
 PA Cargill M, Devlin JJ, Takoubova O;  
 XX WPI; 2004-533949/51.  
 DR N-PSDB; ADQ38813.  
 XX Identifying an individual who has an altered risk for developing  
 PT myocardial infarction by detecting a single nucleotide polymorphism in  
 PT the individual's nucleic acids.  
 XX Claim 10; SEQ ID NO 1304; 145pp; English.  
 PS The invention relates to a novel method for identifying an individual who  
 CC has an altered risk for developing myocardial infarction. The method  
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's  
 CC nucleic acids, where the presence of the SNP is correlated with an  
 CC altered risk for myocardial infarction in the individual. The invention  
 CC further comprises: an isolated nucleic acid molecule comprising at least  
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in  
 CC the specification or its complement and encoding any one of the amino  
 CC acid sequences given in the specification; an isolated polypeptide  
 CC comprising an amino acid sequence given in the specification; an antibody  
 CC that specifically binds to the polypeptide or its antigen-binding  
 CC fragment; an amplified polynucleotide containing an SNP given in the  
 CC specification and which is between about 16 and 1000 nucleotides in  
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
 CC method for identifying an agent useful in treating or preventing  
 CC myocardial infarction. The novel detection method has cardiant activity.  
 CC The nucleic acids of the invention may be used in gene therapy. The  
 CC method is useful in identifying an individual who has an increased or  
 CC decreased risk for developing myocardial infarction and for preparing a  
 CC composition for treating or preventing myocardial infarction. This  
 CC sequence represents the protein of a human myocardial infarction-  
 CC associated gene containing one or more SNP's of the invention. Note: This  
 CC sequence was not shown in the specification. The sequence has come from  
 CC an electronic sequence listing downloaded from the WIPO website.  
 XX  
 SQ Sequence 1089 AA;  
 Query Match 100.0%; Score 5652; DB 8; Length 1089;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGTSHPAFLVGLCLTGLSLILCOLSLPSILPNEKVVQLNSSLRCLFCGSEVSWQYP 60  
 Db 1 MGTSHPAFLVGLCLTGLSLILCOLSLPSILPNEKVVQLNSSLRCLFCGSEVSWQYP 60  
 QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120  
 Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120  
 QY 121 VPDPAVFPGLMGTDLVIVEDDDSAIIPCRRTDPTVTLHNSGVPASVDSRQGFNG 180  
 Db 121 VPDPAVFPGLMGTDLVIVEDDDSAIIPCRRTDPTVTLHNSGVPASVDSRQGFNG 180  
 QY 181 TPTVGPYICEATVKGKGFOTIPFNVALKATSELDLEMEALKTIVYKSGTIVVTCAVFN 240  
 Db 181 TPTVGPYICEATVKGKGFOTIPFNVALKATSELDLEMEALKTIVYKSGTIVVTCAVFN 240  
 QY 241 FVVDLQWTPYGEVKGKGTIMLBEIKVPSIKLVYTLTVPEATVKDSDGYECAAQATREVK 300  
 Db 241 FVVDLQWTPYGEVKGKGTIMLBEIKVPSIKLVYTLTVPEATVKDSDGYECAAQATREVK 300  
 QY 301 EMKKVTISVHEKGFTEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRI SWLKNLTLIENL 360  
 Db 301 EMKKVTISVHEKGFTEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRI SWLKNLTLIENL 360  
 QY 361 TBITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420  
 Db 361 TBITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420  
 QY 421 VDDHSGTGGQVRCCTAEGTPLPDIEWMTCKDIKKCNNTSWTILANNVSNITTEIHSRD 480  
 Db 421 VDDHSGTGGQVRCCTAEGTPLPDIEWMTCKDIKKCNNTSWTILANNVSNITTEIHSRD 480  
 QY 481 RSTVGEGRVTFKVEETIAVRCIAKNLLGAENRELKIVAPTLSELTVAAVLVLLVIVII 540  
 Db 481 RSTVGEGRVTFKVEETIAVRCIAKNLLGAENRELKIVAPTLSELTVAAVLVLLVIVII 540  
 QY 541 SLIVLWVWKQPRYEIRWRVIESISPDGHEIYIYVDPMLQPYDSRWEFFPRDGLVLRVLG 600  
 Db 541 SLIVLWVWKQPRYEIRWRVIESISPDGHEIYIYVDPMLQPYDSRWEFFPRDGLVLRVLG 600  
 QY 601 SGAFKVGEGTAYGLSRSPVWKVAKMLKPTARSEKQALMSSELKIMTHLPHNLINVL 660  
 Db 601 SGAFKVGEGTAYGLSRSPVWKVAKMLKPTARSEKQALMSSELKIMTHLPHNLINVL 660

Db 601 SGAFKGVVEGTAYGLSRSPQWVKVAVKMLKPTARSSEKQALMSSELKIMTHLGLPHLIVNL 660  
QY 661 LGACTKSGPIYIITEYCFYGLDVLNHLKNRDSFLSHPEKPKKELDIFGLNPADESTRSY 720  
Db 661 LGACTKSGPIYIITEYCFYGLDVLNHLKNRDSFLSHPEKPKKELDIFGLNPADESTRSY 720  
QY 721 VILSFENNGDYMOKQADTTQYVPMLEKEVSKYSDIQRSYDRPASYSKKSKMLDSEVKN 780  
Db 721 VILSFENNGDYMOKQADTTQYVPMLEKEVSKYSDIQRSYDRPASYSKKSKMLDSEVKN 780  
QY 781 LLSDDNSEGLTLLDLSFTYQVARGHEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840  
Db 781 LLSDDNSEGLTLLDLSFTYQVARGHEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840  
QY 841 RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLVTTLSDVMSYGILLWEIFSLGCTPPGMM 900  
Db 841 RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLVTTLSDVMSYGILLWEIFSLGCTPPGMM 900  
QY 901 VDSFTFYNKIKSGYMAKPDHATSEVYEIMVKWNSPEKRPSPFYHLSEIVENLLPGQYKK 960  
Db 901 VDSFTFYNKIKSGYMAKPDHATSEVYEIMVKWNSPEKRPSPFYHLSEIVENLLPGQYKK 960  
QY 961 SYEKIHLDFLKSHPAVARVDSNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII 1020  
Db 961 SYEKIHLDFLKSHPAVARVDSNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII 1020  
QY 1021 PLPDIDVPPEEDLGRNHRSSQTSSESATGSSSTFIKREDETIEDIMDDIGIDS 1080  
Db 1021 PLPDIDVPPEEDLGRNHRSSQTSSESATGSSSTFIKREDETIEDIMDDIGIDS 1080  
QY 1081 SLDVEDSFL 1089  
Db 1081 SLDVEDSFL 1089

RESULT 11  
AAR06910  
ID AAR06910 standard; protein; 1089 AA.  
AC AAR06910;  
XX  
XX 25-MAR-2003 (revised)  
DT 16-JAN-1991 (first entry)  
DE Alpha type PDGF receptor deduced from TR4 cDNA clone.  
XX Platelet derived growth factor; T11.  
XX Homo sapiens.  
XX  
XX  
FH Location/Qualifiers  
FT Domain 1..23  
FT /label= signal peptide  
FT Domain 24..524  
FT /label= ligand binding domain  
FT Modified-site 42..44  
FT /label= N-glycos\_site  
FT Modified-site 76..78  
FT /label= N-glycos\_site  
FT Modified-site 103..105  
FT /label= N-glycos\_site  
FT Modified-site 179..181  
FT /label= N-glycos\_site  
FT Modified-site 353..355  
FT /label= N-glycos\_site  
FT Modified-site 359..361  
FT /label= N-glycos\_site  
FT Modified-site 458..460  
FT /label= N-glycos\_site  
FT Modified-site 468..470  
FT /label= N-glycos\_site  
FT Domain 525..548  
FT /label= transmembrane region

FT Domain 549..599  
FT /label= juxtamembrane domain  
FT Binding-site 600..627  
FT /label= ATP binding site  
FT Modified-site 849  
FT /label= tyrosine autophosphorylation site  
XX  
PN W09010013-A.  
XX  
XX 07-SEP-1990.  
XX  
XX 09-FEB-1989; 89US-00308282.  
XX  
XX 09-FEB-1989; 89US-00308282.  
XX  
XX (USDC ) US SEC OF COMMERCE.  
XX (USSH ) US NAT CANCER INST.  
XX  
XX Matsui T, Aaronson SA, Pierce J;  
XX  
XX WPI; 1990-290306/38.  
XX N-PSDB; AAQ05989.  
XX  
XX Type alpha platelet-derived growth factor receptor gene - useful for transforming cells to express novel protein receptor and also susceptible to genetic engineering.  
XX  
XX Claim 7; Fig 3; 64pp; English.  
XX  
XX The TR4 clone is the largest cDNA clone related to the T11 genomic clone, isolated from a library prepd. from human thymus DNA. The T4 cDNA clone was isolated from a M426 human embryo fibroblast cDNA library. The coding region can be introduced into the pSV2 gpt vector with a simian sarcoma virus ITR as a promoter and expressed in a host. The resulting protein is a novel PDGF receptor designated type alpha (the known receptor is designated type beta). The polypeptide has a calculated molecular mass of 120 kD and has all the characteristics of a membrane spanning tyrosine kinase receptor. The extracellular region comprises a hydrophobic signal peptide and a ligand binding domain which has structural homology with the PDGF-R/CSF1-R subfamily. Ten Cys residues are spaced at the same positions as in other receptors of the sub-family and eight potential N-linked glycosylation sites are also present. A hydrophobic segment spans the membrane and the cyto-plasmic region comprises a juxtamembrane region, a tyrosine kinase region split into TK1 and TK2 by a hydrophilic interkinase region and a hydrophilic C-terminal tail. The TK region includes the consensus ATP binding sequence (G-X-G-X-X-G..X) and a tyrosine autophosphorylation site homologous to that of pp60(v-src). (Updated on 25-MAR-2003 to correct PA field.)  
XX  
XX Sequence 1089 AA;  
SQ  
Query Match 99.9%; Score 5649; DB 2; Length 1089;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGTSHPAFLVGLCLTGLSLILCOLSLPSILPNEKVKVQLNSFSLRCFGESEVSWQYP 60  
Db 1 MGTSHPAFLVGLCLTGLSLILCOLSLPSILPNEKVKVQLNSFSLRCFGESEVSWQYP 60  
QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENLEGRHIYY 120  
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENLEGRHIYY 120  
QY 121 VPDPOVAFVPLGMDTYLVIVVEDDDSAIICRTTDPETPTVTLHNSGVVPASYSROGFNG 180  
Db 121 VPDPOVAFVPLGMDTYLVIVVEDDDSAIICRTTDPETPTVTLHNSGVVPASYSROGFNG 180  
QY 181 TPTVGPYICEATVKGKKFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
Db 181 TPTVGPYICEATVKGKKFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
QY 241 EYVDLQWTFPGEVKGKGITMLEEIKVPSIKLVYTLVTPVATVKSDGDECAAPQATREVK 300  
Db 241 EYVDLQWTFPGEVKGKGITMLEEIKVPSIKLVYTLVTPVATVKSDGDECAAPQATREVK 300

Db 241 EVVDLQWTFGEVKGIGITMLEBIKVPISIKLVYTLTVPEATVKDSDGYEACAAQATREVK 300  
Qy 301 EMKVVTSVHEKGFIEIKPTFSOLEAVNLHEVGHVVEVAYPPRISWLNKNTLILENL 360  
Db 301 EMKVVTSVHEKGFIEIKPTFSOLEAVNLHEVGHVVEVAYPPRISWLNKNTLILENL 360  
Qy 361 TEITTDVEKIQTIRYRSKLIIRAKBEDSDHYITVAQNEADVKSFTFELLTQVPSILDL 420  
Db 361 TEITTDVEKIQTIRYRSKLIIRAKBEDSDHYITVAQNEADVKSFTFELLTQVPSILDL 420  
Qy 421 VDDHSGTGQTVRCTAEGTLPDIEMWICKDKCNNETSWITLANNVSNITIEHSRD 480  
Db 421 VDDHSGTGQTVRCTAEGTLPDIEMWICKDKCNNETSWITLANNVSNITIEHSRD 480  
Qy 481 RSTVEGRVTFKVBETIARVCLAKNLLGAENRELKVAPTLRSELTVAAAVLVLLVIVII 540  
Db 481 RSTVEGRVTFKVBETIARVCLAKNLLGAENRELKVAPTLRSELTVAAAVLVLLVIVII 540  
Qy 541 SLIVLVVWIKQKPRYERIRNRVIESISPDGHEIYVDPQMLPYDSRWEFFPRDGLVLRVLG 600  
Db 541 SLIVLVVWIKQKPRYERIRNRVIESISPDGHEIYVDPQMLPYDSRWEFFPRDGLVLRVLG 600  
Qy 601 SGAFKGVVEGTAYGLSRQPMKVAVKMLKPTARSSEKQALMSSELKIMTHLGPLHNLVNL 660  
Db 601 SGAFKGVVEGTAYGLSRQPMKVAVKMLKPTARSSEKQALMSSELKIMTHLGPLHNLVNL 660  
Qy 661 LGACTKSGPIYIITEYCFYGDVLYNLHKNRDSFLSHPEKPKKELDI FGLNPADESTRSY 720  
Db 661 LGACTKSGPIYIITEYCFYGDVLYNLHKNRDSFLSHPEKPKKELDI FGLNPADESTRSY 720  
Qy 721 VILSFENNNGDYMDMKQADTTQYVPMLEKEVSKYSIDIQSLYDRPASYSKKKMLDSEVKX 780  
Db 721 VILSFENNNGDYMDMKQADTTQYVPMLEKEVSKYSIDIQSLYDRPASYSKKKMLDSEVKX 780  
Qy 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKKNCVHRDLAARNVLLAQKIVKICDFGLA 840  
Db 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKKNCVHRDLAARNVLLAQKIVKICDFGLA 840  
Qy 841 RDIHDSNVYSKSGTFLPVKWMAPESIFDNLTYTLSDVMSYGILLWEIIFSLGCTPYPGMW 900  
Db 841 RDIHDSNVYSKSGTFLPVKWMAPESIFDNLTYTLSDVMSYGILLWEIIFSLGCTPYPGMW 900  
Qy 901 VDSFTFNKIKSGYRMAKPDHATSEVVEIMVKNSEPEKPSFYHLSEIVENLLPQYKK 960  
Db 901 VDSFTFNKIKSGYRMAKPDHATSEVVEIMVKNSEPEKPSFYHLSEIVENLLPQYKK 960  
Qy 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNBEDKLKDWEGGLDEORLSADSGYII 1020  
Db 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNBEDKLKDWEGGLDEORLSADSGYII 1020  
Qy 1021 PLPDIDPVPEEDLGRNHRSSQTSSESALETGSSSTFIKREDETIEDIDMDDIGIDS 1080  
Db 1021 PLPDIDPVPEEDLGRNHRSSQTSSESALETGSSSTFIKREDETIEDIDMDDIGIDS 1080  
Qy 1081 SLDVDSFL 1089  
Db 1081 SLDVDSFL 1089

RESULT 12  
ABG72453  
ID ABG72453 standard; protein; 1089 AA.

XX ABG72453;

XX 13-FEB-2003 (first entry)

DE Human platelet derived growth factor receptor alpha mutant V859M.

XX Human; platelet derived growth factor receptor alpha; PDGFRalpha;  
KW hepatocytic; dermatological; nephrotropic; vulnarary; opthamological;  
KW cytotatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;  
KW phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;

KW cell migration; extracellular matrix synthesis; secretion;  
KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;  
KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;  
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;  
XX mutant; mutein.

OS Homo sapiens.

OS Synthetic.

XX Key

FT Domain 1. .490

FT Peptide 1. .24

FT Peptide 1. .20

FT Protein 21

FT Protein 25

FT Domain 42. .102

FT Domain 143. .191

FT Domain 228. .292

FT Domain 338. .399

FT Domain 428. .503

FT Domain 525. .548

FT Domain 549. .1055

FT Domain 556. .661

FT Domain 760. .900

FT Misc-difference 859

XX US2002111304-A1.

XX 15-AUG-2002.

XX 25-MAY-2001; 2001US-00866510.

XX 01-DEC-2000; 2000US-0250747F.

XX 07-MAY-2001; 2001US-0289103P.

XX (KAZL/) KAZLAUSKAS A.

XX (IKUN/) IKUNO Y.

XX Kazlauskas A, Ikuno Y;

XX WPI: 2003-066697/06.

XX N-PSDB; ABS57784.

XX New polypeptide for treating or preventing diseases associated with an

XX abnormal platelet-derived growth factor (PDGF) level, e.g. cell

XX proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha

XX or -beta.

XX Claim 7; Page 64-67; 127pp; English.

XX The invention describes a polypeptide comprising a portion of the

XX receptor tyrosine kinase platelet-derived growth factor alpha receptor

XX (PDGFalphaR). The polypeptide and the polynucleotide are useful in

XX treating or preventing diseases and conditions associated with an

XX abnormal PDGF level or response, such as cell proliferation, cell

XX migration, extracellular matrix synthesis and secretion or cell

XX contraction. Exemplary diseases or disorders include cell proliferative



/note= "Split tyrosine kinase domain segment 2"

US2002111304-A1.

15-AUG-2002.

25-MAY-2001; 2001US-00866510.

01-DEC-2000: 2000US-0250747P.

07-MAY-2001; 2001US-0289103P.

A (KAZL/) KAZLAUSKAS A.  
A (IKTN/) IKTNO V

Y  
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R N-PSDB; ABS57781.

New polypeptide fo

abnormal platelet-derived growth factor (PDGF) levels, e.g. cell proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha or -beta.

Claim 7: Page 45-47: 127pp: English.

The invention describes a polypeptide comprising a portion of the

receptor tyrosine kinase platelet-derived growth factor alpha receptor (PDGFR- $\alpha$ ) the neuropeptide and the neuropeptide analogs in

treating or preventing diseases and

migration, extracellular matrix synthesis and secretion or cell contraction. Exemplary diseases or disorders include cell proliferative diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g. atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis, scleroderma, keloids, hypertrophic scars, skin wound healing or proliferative vitreoretinopathy). The method may be used in identifying compounds for treating or preventing the development of diseases involving cell contraction, e.g. fibrotic diseases. This is the amino acid sequence of human platelet derived growth factor receptor (PDGFR) alpha mutant E587K

Sequence 1089 AA:

Query Match

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1000. Concentration 1.0. Mismatches 0.0. Indels 0.0. Cons

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[illegible]

61 MSEESSDVEIRNEENNGLFVTVLEVVSSASAAHTGLYTCYYNHTQTEENELEGRHIYI

61 MSEEESDVEIRNEENNGLFVTVLEVSSASAHTGLYTCYNNHTQTEENELEGRHIYI I

121 VPDPDVAFVPLGMTDYLVIIVEDDDSAIIPCRITDPETPTLHNSGVVPASYSRQGFNG 1

121 VPDPDVAFVPLGMTDYLIVEDDDSAIIPCRITDPETPTLHNSEGVPASYSRQGFNG 1

181 T F T V G P Y I C E A T V K G K K F Q T I P F N V Y A L K A T S E L D L E M E A L K T V Y K S G E T I V V T C A V F N N 2

181 TFTVGPYICEATVKGKFKQIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVFN 2

241 EVVDLOWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSDGYECAAROATREVK 3

241 EWWRIOWTYPGEVKGKGI.TMI.EEIKVPSTKI.VYTI.TVPEATVKDSDYECABROATREVK 3

301 5M2K4T1C1U5K5C6T1P1V0P5C01 P1A1N1Y H5Y1W4J5E1D1E1W1B1A1V0D0D0T1C0W1 V1A1N1T1T1 T1E1N1T1 2

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Db	361	TEITDTTDEKIQEIRYSKGLIRAKEBDSGHYITVAQNEDAVKSYTFELLTQVPSLIDL	420
Qy	421	VDDHGGSTGGTQVRCCTAEGTLPDIEWMI CKDIKKCNNETSWTILANNVSNII TEIHSRD	480
Db	421	VDDHGGSTGGTQVRCCTAEGTLPDIEWMI CKDIKKCNNETSWTILANNVSNII TEIHSRD	480
Qy	481	RSTVEGRVTFAKVBETIAVRCLAKNLGAENREIKLVAPTURSELTVAAAVLLVLVII	540
Db	481	RSTVEGRVTFAKVBETIAVRCLAKNLGAENREIKLVAPTURSELTVAAAVLLVLVII	540
Qy	541	SLIVLVWIKQPKRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWKFPDGLVLRVLG	600
Db	541	SLIVLVWIKQPKRYEIRWRVIESISPDGHEYIYVDPMLPYDSRWKFPDGLVLRVLG	600
Qy	601	SGAFGKVEGTAYGLSRSQPMKVAVKMLKPTARSSKQALMSELKIMTHLGPLHNI VNL	660
Db	601	SGAFGKVEGTAYGLSRSQPMKVAVKMLKPTARSSKQALMSELKIMTHLGPLHNI VNL	660
Qy	661	LGACTKSGPIYIITEYCFYGDVNLVYLNHKNRDSFLSHPEKPKKELDFGLNPADESTSY	720
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Qy	721	VILSFENNGDYMDMKQADTTQYVPMLEKESKYSDIQRSLYDRPASYYKKKSMLDSEVKN	780
Db	721	VILSFENNGDYMDMKQADTTQYVPMLEKESKYSDIQRSLYDRPASYYKKKSMLDSEVKN	780
Qy	781	LLSDNSEGLTLLDLLSFTTQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LLSDNSEGLTLLDLLSFTTQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Qy	841	RDIMHDSNYYSKGSTFLPVKWMAPESIFDNLVYTLSDVWSYGILLWEIFSLGGTYPGCM	900
Db	841	RDIMHDSNYYSKGSTFLPVKWMAPESIFDNLVYTLSDVWSYGILLWEIFSLGGTYPGCM	900
Qy	901	VDSTFYNKIKSGYRNMAKPDHATSEVYIMVKWCNNESEKPSFVYHLSEIVENLLPGQYKK	960
Db	901	VDSTFYNKIKSGYRNMAKPDHATSEVYIMVKWCNNESEKPSFVYHLSEIVENLLPGQYKK	960
Qy	961	SYEKIHDLFLKSDHPAVARMVDSDNAYIGVYTKNEEDKLKWEGGLDEQRLSADSGYII	1020
Db	961	SYEKIHDLFLKSDHPAVARMVDSDNAYIGVYTKNEEDKLKWEGGLDEQRLSADSGYII	1020
Qy	1021	PLPDIDVPVEEDLKGKRNHSSQTSSESAIETGSSSTFIKREDETIEDIMDDIDIGDS	1080
Db	1021	PLPDIDVPVEEDLKGKRNHSSQTSSESAIETGSSSTFIKREDETIEDIMDDIDIGDS	1080
Qy	1081	SDLVEDSFL 1089	
Db	1081	SDLVEDSFL 1089	
RESULT 14			
ABG72452			
ID	ABG72452 standard; protein; 1089 AA.		
XX	AC ABG72452;		
XX	AC ABG72452;		
DT	13-FEB-2003 (first entry)		
XX	DE Human platelet derived growth factor receptor alpha mutant D818N.		
KW	Human; platelet derived growth factor receptor alpha; PDGFalpha;		
KW	hepatotropic; dermatological; nephrotropic; vulnary; ophthalmological;		
KW	cytostatic; gene therapy; vaccine; phosphoinositide-kinase-inhibitor-3;		
KW	phospholipase-inhibitor-C; receptor tyrosine kinase; cell proliferation;		
KW	cell migration; extracellular matrix synthesis; secretion;		
KW	cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;		
KW	liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;		
KW	keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;		
XX	mutant; muten.		
XX	XX		
OS	Homo sapiens.		

OS Synthetic.  
XX Key Location/Qualifiers  
FT Domain 1. .490  
FT /label= Extracellular\_domain  
FT Peptide 1. .24  
FT /label= Signal\_peptide\_sequence\_2  
FT Peptide 1. .20  
FT /label= Signal\_peptide\_sequence\_1  
FT Protein 21  
FT /label= Mature\_PDGRF\_sequence\_1  
FT Protein 25  
FT /label= Mature\_PDGRF\_sequence\_2  
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FT Domain 143. .191  
FT /label= Immunoglobulin-like\_domain  
FT Domain 228. .292  
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FT Domain 338. .399  
FT /label= Immunoglobulin-like\_domain  
FT /note= "6"  
FT Domain 428. .503  
FT /label= Immunoglobulin-like\_domain  
FT Domain 525. .548  
FT /label= Transmembrane\_domain  
FT Domain 549. .1055  
FT /label= Intracellular\_domain  
FT Domain 556. .661  
FT /note= "Split tyrosine kinase domain segment 1"  
FT Domain 760. .900  
FT /note= "Split tyrosine kinase domain segment 2"  
FT Misc-difference 818  
FT /note= "Wild type Asp substituted by Asn"  
XX  
PN US2002111304-A1.  
XX  
PD 15-AUG-2002.  
XX  
XX 25-MAY-2001; 2001US-00866510.  
PR 01-DEC-2000; 2000US-0250747P.  
PR 07-MAY-2001; 2001US-0289103P.  
XX  
PA (KAZL/) KAZLAUSKAS A.  
PA (IKUN/) IKUNO Y.  
XX  
PI Kazlauskas A, Ikuno Y;  
XX  
XX WPI; 2003-066697/06.  
DR N-PSDB; ABS57783.  
XX  
XX New polypeptide for treating or preventing diseases associated with an  
PT abnormal platelet-derived growth factor (PDGF) level, e.g. cell  
PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha  
PT or -beta.  
XX  
PS Claim 7; Page 58-60; 127pp; English.  
XX  
XX The invention describes a polypeptide comprising a portion of the  
CC receptor tyrosine kinase platelet-derived growth factor alpha receptor  
CC (PDGFalpha). The polypeptide and the polynucleotide are useful in  
CC treating or preventing diseases and conditions associated with an  
CC abnormal PDGF level or response, such as cell proliferation, cell  
CC migration, extracellular matrix synthesis and secretion or cell  
CC contraction. Exemplary diseases or disorders include cell proliferative  
CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.  
CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,  
CC scleroderma, keloids, hypertrophic scars, skin wound healing or  
CC proliferative vitreoretinopathy). The method may be used in identifying  
CC compounds for treating or preventing the development of diseases  
CC involving cell contraction, e.g. fibrotic diseases. This is the amino  
CC acid sequence of human platelet derived growth factor receptor (PDGFR)

CC	alpha mutant D818N	
XX		
SQ	Sequence 1089 AA;	
	Query Match 99.9%; Score 5647; DB 6; Length 1089;	
	Best Local Similarity 99.9%; Pred. No. 0;	
	Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP	60
DB	1 MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP	60
QY	61 MSEEESDVEIRNEENNNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELGRHIYY	120
DB	61 MSEEESDVEIRNEENNNSGLFVTVLEVSSASAAHTGLTYTCYNHTQTEENELGRHIYY	120
QY	121 VDDPDVAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASVDSROGFNG	180
DB	121 VDDPDVAFVPLGMDYLVIVEDDDSAIIPCRITDPTPTVTLHNSGVVPASVDSROGFNG	180
QY	181 TTTVGPYICEATVKGKFKQTIPFNYYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
DB	181 TTTVGPYICEATVKGKFKQTIPFNYYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
QY	241 EVVDLQWTPGGEVKGKGIITMLBEIKVPSIKLVTVTLVPEATVKDSDGYECAARQATREVK	300
DB	241 EVVDLQWTPGGEVKGKGIITMLBEIKVPSIKLVTVTLVPEATVKDSDGYECAARQATREVK	300
QY	301 EMKKVTISVHEKGFIEIKPTFSOLEAVNLHEVKHFVVEVRAVPPRISLWKNLTLLENL	360
DB	301 EMKKVTISVHEKGFIEIKPTFSOLEAVNLHEVKHFVVEVRAVPPRISLWKNLTLLENL	360
QY	361 TEITTDVEKIQEIYRSKLVKLRKEEDSGHYITVAQNEADAVKSYTFELLTQVPSISLDL	420
DB	361 TEITTDVEKIQEIYRSKLVKLRKEEDSGHYITVAQNEADAVKSYTFELLTQVPSISLDL	420
QY	421 VDDHGGSTGGQVRCVTAEGTPIPDIEWMI CKDKKCNNETSWTILANNVSNITIEHSRD	480
DB	421 VDDHGGSTGGQVRCVTAEGTPIPDIEWMI CKDKKCNNETSWTILANNVSNITIEHSRD	480
QY	481 RSTVEGRVTFAKVEETIAVRCIAKLNLLGAENRELKLVAPTLRSELTVAAAVLVLLVII	540
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QY	541 SLIVLVIIWKQKPRYRIRWRVIESISPDGHEIYIVDPMQLPYDSRWEFFPRDGLVLRVLG	600
DB	541 SLIVLVIIWKQKPRYRIRWRVIESISPDGHEIYIVDPMQLPYDSRWEFFPRDGLVLRVLG	600
QY	601 SGAFGKVEGTAYGLSRSPQVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL	660
DB	601 SGAFGKVEGTAYGLSRSPQVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL	660
QY	661 LGACTKSGPIYIITEYCFYGDVLYLHKNRDPSFLSHHPEKPKKELDIFGLNPADESTRSY	720
DB	661 LGACTKSGPIYIITEYCFYGDVLYLHKNRDPSFLSHHPEKPKKELDIFGLNPADESTRSY	720
QY	721 VILSFENNGDYMDMKQADTTQVVPMLERKEVSKYSDIQRSLYDRPASYYKKKSLMDSSEVK	780
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QY	781 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNVCVHRDLAARNVLLAQGKIVKICDFGLA	840
DB	781 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNVCVHRDLAARNVLLAQGKIVKICDFGLA	840
QY	841 RDMHDSNVKSGSTFLPVKMWAPESIFDNLYTTLSDVMSYGILLMEIFSLGGTTPYGMW	900
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QY	901 VDSFTFNKIKSGYMAKPDHATSEVYEIMVCKWNSPEKRPSPFYHLSEIVENLLPGQYKK	960
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QY	961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTYTKNEEDKLKDWEGGLDEQRLSADSGYII	1020





QY	481	RSTVEGRVTF	AKVEETIAVRCLAKNLLGAENRELKLVAPT	LRSELTVAAAVLLVIVII	540	
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Db	481	RSTVEGRVTF	AKVEETIAVRCLAKNLLGAENRELKLVAPT	LRSELTVAAAVLLVIVII	540	
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Db	601	SGAFKGVVEGTAY	GLSRSPVMKVAVMKMLKPTAR	SEKQALMSELKIMTHLGP	HLNIVNL 660	
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QY	721	VILSFENNGDYM	DKQADTTQYVPMLE	RKESVSKYSDIQ	RSLYDRPASYYKKSM	LDSEVKN 780
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QY	781	LLSDDNSEGL	TLDDLSTFYQVARGMEF	LASKNCVHRDLAARNV	LLAQGKI	VKICDFGLA 840
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QY	1081	SDLVEDSFL	1089			
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Job time : 134.505 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2005, 07:10:35 ; Search time 31.7522 Seconds  
(without alignments)  
2560.230 Million cell updates/sec

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Perfect score: 5652  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5652	100.0	1089	1	US-08-168-917-4
2	5652	100.0	1089	2	US-08-460-510-4
3	5652	100.0	1089	2	US-08-460-490-4
4	5652	100.0	1089	3	US-08-462-728-2
5	5652	100.0	1089	3	US-08-461-917-2
6	5652	100.0	1089	4	US-08-464-436-2
7	5652	100.0	1089	4	US-08-464-436-2
8	5652	100.0	1089	4	US-09-769-987-2
9	5652	100.0	1089	4	US-09-866-510-2
10	5652	100.0	1089	4	US-09-919-497-90
11	5652	100.0	1089	4	US-09-949-016-6703
12	5652	100.0	1089	5	PCT-US92-00730-4
13	5652	100.0	1089	5	PCT-US92-00862-4
14	5649	99.9	1089	4	US-09-866-510-10
15	5648	99.9	1089	1	US-08-180-195-36
16	5648	99.9	1089	1	US-08-477-329-36
17	5648	99.9	1089	2	US-08-475-458-36
18	5648	99.9	1089	3	US-08-980-400-36
19	5648	99.9	1089	3	US-09-583-459A-36
20	5648	99.9	1089	3	US-09-583-210-36
21	5648	99.9	1089	3	US-09-583-449A-36
22	5648	99.9	1089	3	US-09-435-059-36
23	5648	99.9	1089	4	US-09-866-510-8
24	5647	99.9	1089	4	US-09-866-510-8
25	5646	99.9	1089	4	US-09-866-510-6
26	5636.5	99.7	1088	4	US-09-961-403-4
27	3560.5	63.0	762	4	US-09-949-016-7568

28	3046	53.9	589	4	US-09-866-510-12	Sequence 12, Appl
29	2354.5	41.7	1106	1	US-08-180-195-2	Sequence 2, Appl
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34	2354.5	41.7	1106	3	US-09-583-210-2	Sequence 2, Appl
35	2354.5	41.7	1106	3	US-09-583-449A-2	Sequence 2, Appl
36	2354.5	41.7	1106	3	US-09-435-059-2	Sequence 2, Appl
37	2354.5	41.7	1106	4	US-09-866-510-22	Sequence 22, Appl
38	2351.5	41.6	1106	1	US-08-168-917-2	Sequence 2, Appl
39	2351.5	41.6	1106	2	US-08-460-510-2	Sequence 2, Appl
40	2351.5	41.6	1106	2	US-08-460-490-2	Sequence 2, Appl
41	2351.5	41.6	1106	3	US-08-462-728-4	Sequence 4, Appl
42	2351.5	41.6	1106	3	US-08-461-917-4	Sequence 4, Appl
43	2351.5	41.6	1106	4	US-08-464-436-4	Sequence 4, Appl
44	2351.5	41.6	1106	4	US-08-464-436-4	Sequence 4, Appl
45	2351.5	41.6	1106	5	PCT-US92-00730-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-168-917-4  
; Sequence 4, Application US/08168917  
; Patent No. 5686572  
; GENERAL INFORMATION:  
; APPLICANT: Wolf, David  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: Fretto, Larry J.  
; APPLICANT: Giese, Neill A.  
; APPLICANT: Escobedo, Jaime A.  
; APPLICANT: Williams, Lewis T.  
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND AND TOWNSEND  
; STREET: Stewart Street Tower, 20th Floor \ One Market  
; STREET: Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,917  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/650,793  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: 12418-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1089 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-168-917-4

Query Match 100.0%; Score 5652; DB 1; Length 1089;

Best Local Similarity 100.0%; Pred. No. 0;		Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1	MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP	60
QY	61	MSEESDVIRNEENNSGLFVTLEVSASAAHTGLTYCYNNHTQTEENELGRIIY	120
Db	61	MSEESDVIRNEENNSGLFVTLEVSASAAHTGLTYCYNNHTQTEENELGRIIY	120
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Db	121	VPDPVAFVPLGMDTLVIVEDDSDAIIPCRITDPTPTVTLHNSGVWPASYSRQGFNG	180
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Db	181	TFTVGPYICEATVKGKFKQTIPNNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
QY	241	EVVDLQWTPGEGVKGIGITMLBEIKVPSIKLVYTLVPEATVKDSDGYECAARQATREVK	300
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Db	361	TEITDVEKIQETIRYSKLIIRAKEDSGHYITVAQNEADVAKSYTFELLTQVPSILD	420
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QY	481	RSTVEGRVTPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII	540
Db	481	RSTVEGRVTPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII	540
QY	541	SLIVLVVINKQPRYIRRWVIESIPDGHYIYVDPMQLPYDSRWEFFRDGLVGRVLG	600
Db	541	SLIVLVVINKQPRYIRRWVIESIPDGHYIYVDPMQLPYDSRWEFFRDGLVGRVLG	600
QY	601	SGAFGKVEGTAYGLRSQVPMKAVKMLKPTARSSEKQALMSSELKIMTHLGHPLINVL	660
Db	601	SGAFGKVEGTAYGLRSQVPMKAVKMLKPTARSSEKQALMSSELKIMTHLGHPLINVL	660
QY	661	LGACTKSGPIYIITEYCFYGDLYNHLKNRDPSFLSHHPEKPKKELDIFGLNPADESTSY	720
Db	661	LGACTKSGPIYIITEYCFYGDLYNHLKNRDPSFLSHHPEKPKKELDIFGLNPADESTSY	720
QY	721	VILSFENNGDYMCKQADTTQYVPMLEKRVSKYSDIQSLYDRPASYKKSMLDSEVKN	780
Db	721	VILSFENNGDYMCKQADTTQYVPMLEKRVSKYSDIQSLYDRPASYKKSMLDSEVKN	780
QY	781	LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
Db	781	LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
QY	841	RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGTPPGMM	900
Db	841	RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGTPPGMM	900
QY	901	VDSTFYNNKIKSGYRMKPDHATSEVVEIMVKWNSPEKPSFYHSEIVENLLPGQYKK	960
Db	901	VDSTFYNNKIKSGYRMKPDHATSEVVEIMVKWNSPEKPSFYHSEIVENLLPGQYKK	960
QY	961	SYEKIHLDFLKSHPAVARMRVSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII	1020
Db	961	SYEKIHLDFLKSHPAVARMRVSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII	1020
QY	1021	PLPDIDPVEEDLGKKNRHSSQTSBESALETGSSSSTFIKREDETIEDIDMDDIGIDS	1080

Db	1021	PLPDIDPVEEDLGKKNRHSSQTSBESALETGSSSSTFIKREDETIEDIDMDDIGIDS	1080
QY	1081	SDLVDSFL	1089
Db	1081	SDLVDSFL	1089
RESULT 2			
US-08-460-510-4			
; Sequence 4, Application US/08460510			
; Patent No. 5872218			
; GENERAL INFORMATION:			
; APPLICANT: Wolf, David			
; APPLICANT: Tomlinson, James E.			
; APPLICANT: Fretto, Larry J.			
; APPLICANT: Giese, Neill A.			
; APPLICANT: Escobedo, Jaime A.			
; APPLICANT: Williams, Lewis T.			
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN			
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES			
; NUMBER OF SEQUENCES: 23			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW			
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: US			
; ZIP: 94105			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/460,510			
; FILING DATE: 02-JUN-1995			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Dow, Karen B.			
; REGISTRATION NUMBER: 29,684			
; REFERENCE/DOCKET NUMBER: 012418-001430			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 326-2400			
; TELEFAX: (415) 326-2422			
; INFORMATION FOR SEQ ID NO: 4:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1089 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-460-510-4			
Query Match 100.0%; Score 5652; DB 2; Length 1089;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP	60
Db	1	MGTSHPAFLVGLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP	60
QY	61	MSEESDVIRNEENNSGLFVTLEVSASAAHTGLTYCYNNHTQTEENELGRIIY	120
Db	61	MSEESDVIRNEENNSGLFVTLEVSASAAHTGLTYCYNNHTQTEENELGRIIY	120
QY	121	VPDPVAFVPLGMDTLVIVEDDSDAIIPCRITDPTPTVTLHNSGVWPASYSRQGFNG	180
Db	121	VPDPVAFVPLGMDTLVIVEDDSDAIIPCRITDPTPTVTLHNSGVWPASYSRQGFNG	180
QY	181	TFTVGPYICEATVKGKFKQTIPNNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
Db	181	TFTVGPYICEATVKGKFKQTIPNNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN	240
QY	241	EVVDLQWTPGEGVKGIGITMLBEIKVPSIKLVYTLVPEATVKDSDGYECAARQATREVK	300

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Db 241 EVVDLQWTPGVEYKGIIMLEIKVPSIKLVYTLVPEATVKDSDGYECAARQATREVK 300
Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVEKHFVVEVRAYPPIPRISMLKNLTLIENL 360
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVEKHFVVEVRAYPPIPRISMLKNLTLIENL 360
Qy 361 TEITTDVEKIQEIRYSKLIIRAKEDSDGHTYIVAQNEDAVKSYTFELLTQVPSIIDL 420
Db 361 TEITTDVEKIQEIRYSKLIIRAKEDSDGHTYIVAQNEDAVKSYTFELLTQVPSIIDL 420
Qy 421 VDDHGSTGGQVTRCTAEGTLPDIEMWICKD1KCCNNETSWTLANNVSNITTEIHSRD 480
Db 421 VDDHGSTGGQVTRCTAEGTLPDIEMWICKD1KCCNNETSWTLANNVSNITTEIHSRD 480
Qy 481 RSTVEGRVTFAKVEETIAVRCIAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db 481 RSTVEGRVTFAKVEETIAVRCIAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Qy 541 SLIVLVVWVKQKPRYRIRWRVIES1SPDGHEIYIVDPMQLPYDSRWEPFRDGLVLRVLG 600
Db 541 SLIVLVVWVKQKPRYRIRWRVIES1SPDGHEIYIVDPMQLPYDSRWEPFRDGLVLRVLG 600
Qy 601 SGAFGVVEGTAYGLSRSPQVMKAVKMLKPTARSSEKQALMSELKIMTHLGHPLINVL 660
Db 601 SGAFGVVEGTAYGLSRSPQVMKAVKMLKPTARSSEKQALMSELKIMTHLGHPLINVL 660
Qy 661 LGACTKSGPIIITEYCFYGDVLYNLHKRDSFLSHHPKPKKELDIFGLNPADESTRSY 720
Db 661 LGACTKSGPIIITEYCFYGDVLYNLHKRDSFLSHHPKPKKELDIFGLNPADESTRSY 720
Qy 721 VILSPENNGDYMDKQADTTQYVPMLEKREVKYSID1QRLSYDRPASYKKKSMLDSEVKN 780
Db 721 VILSPENNGDYMDKQADTTQYVPMLEKREVKYSID1QRLSYDRPASYKKKSMLDSEVKN 780
Qy 781 LLSDDNSEGLTLLDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db 781 LLSDDNSEGLTLLDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy 841 RDIHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTPYPGWM 900
Db 841 RDIHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTPYPGWM 900
Qy 901 VDSFTFNKIKSGYMAKPDHATSEVTEIMVKCNSEPEKPSFYHLSEIVENLLPGQYKK 960
Db 901 VDSFTFNKIKSGYMAKPDHATSEVTEIMVKCNSEPEKPSFYHLSEIVENLLPGQYKK 960
Qy 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDEORLSADSGYII 1020
Qy 1021 PLPDIDPVEEDLGRNHSSTSESASETSSSTFKREDETIEDIDMDDIGIDS 1080
Db 1021 PLPDIDPVEEDLGRNHSSTSESASETSSSTFKREDETIEDIDMDDIGIDS 1080
Qy 1081 SLDVEDSFL 1089
Db 1081 SLDVEDSFL 1089
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## RESULT 3

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US-08-460-490-4
; Sequence 4, Application US/08460490
; Patent No. 5891652
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
```

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; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,490
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-490-4
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Query Match 100.0%; Score 5652; DB 2; Length 1089;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSHPAFLVGLCLTGLSLILCOLSLPILPNEKVVQLNSSFSLRCFGESEVSNQYP 60
Db 1 MGTSHPAFLVGLCLTGLSLILCOLSLPILPNEKVVQLNSSFSLRCFGESEVSNQYP 60
Qy 61 MSEEESDVEIRNEENNSGLFVTLEVSASAHTGLTYCYNHTQTEENELEGRHIYI 120
Db 61 MSEEESDVEIRNEENNSGLFVTLEVSASAHTGLTYCYNHTQTEENELEGRHIYI 120
Qy 121 VPDVDVAFVPLGMDTVLIVVEDDDSAIIPCRTTDPETPTVLHNSGVVPASYSRQGFNG 180
Db 121 VPDVDVAFVPLGMDTVLIVVEDDDSAIIPCRTTDPETPTVLHNSGVVPASYSRQGFNG 180
Qy 181 TPTVGPYICEATVKGKGFQIIPENVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 240
Db 181 TPTVGPYICEATVKGKGFQIIPENVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 240
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Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVEKHFVVEVRAYPPIPRISMLKNLTLIENL 360
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Qy 361 TEITTDVEKIQEIRYSKLIIRAKEDSDGHTYIVAQNEDAVKSYTFELLTQVPSIIDL 420
Db 361 TEITTDVEKIQEIRYSKLIIRAKEDSDGHTYIVAQNEDAVKSYTFELLTQVPSIIDL 420
Qy 421 VDDHGSTGGQVTRCTAEGTLPDIEMWICKD1KCCNNETSWTLANNVSNITTEIHSRD 480
Db 421 VDDHGSTGGQVTRCTAEGTLPDIEMWICKD1KCCNNETSWTLANNVSNITTEIHSRD 480
Qy 481 RSTVEGRVTFAKVEETIAVRCIAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db 481 RSTVEGRVTFAKVEETIAVRCIAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Qy 541 SLIVLVVWVKQKPRYRIRWRVIES1SPDGHEIYIVDPMQLPYDSRWEPFRDGLVLRVLG 600
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Db 541 SLVLVVIWKQPRYIRWRVIESIPDGHYIYVDPMLPYDSRWEFFRDLGLVLRGLG 600  
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Db 661 LGACTKSGPIYIITEYCFYGDVLYLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
QY 721 VILSFENNGDYMCKQADTTQYVPMLEKEVSKYDIQRSLYDRPASYYKKSMLDSEVKX 780  
Db 721 VILSFENNGDYMCKQADTTQYVPMLEKEVSKYDIQRSLYDRPASYYKKSMLDSEVKX 780  
QY 781 LLSDDNSEGLTLLDLISFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840  
Db 781 LLSDDNSEGLTLLDLISFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840  
QY 841 RDIHDSNVYKSGSTFLPVKMAPEISFDNLYTTLSGVMSYGILLWEIFSLGCTPYPGMM 900  
Db 841 RDIHDSNVYKSGSTFLPVKMAPEISFDNLYTTLSGVMSYGILLWEIFSLGCTPYPGMM 900  
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Db 901 VDSFTFYNKIKSGYMAKPDHATSEVYIEMVKWNSPEKRPSPFYHLSEIVENLLPGQYKX 960  
QY 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTTYKNEEDKLKOWEGGLDRORLSADSGYII 1020  
Db 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTTYKNEEDKLKOWEGGLDRORLSADSGYII 1020  
QY 1021 PLFDIPVPEEDLGKRNHSSQTSBESAIETGSSSTFKRDETIEDIDMDDIGIDS 1080  
Db 1021 PLFDIPVPEEDLGKRNHSSQTSBESAIETGSSSTFKRDETIEDIDMDDIGIDS 1080  
QY 1081 SLDVEDSFL 1089  
Db 1081 SLDVEDSFL 1089

RESULT 4  
US-08-462-728-2  
; Sequence 2, Application US/08462728  
; Patent No. 6043211  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, Lewis T.  
; APPLICANT: ESCOBEDO, Jaime A.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market, Steuart Street Tower, 20th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462, 728  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/309,322  
; FILING DATE: 10-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/151,414  
; FILING DATE: 02-FEB-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.

; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 2307K-267-2-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/326-2400  
; TELEFAX: 415/326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1089 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-462-728-2  
Query Match 100.0%; Score 5652; DB 3; Length 1089;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 MSEEESDDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNNHTQTEENLEGRHIYI 120  
Db 61 MSEEESDDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNNHTQTEENLEGRHIYI 120  
QY 121 VPDPDVAFVPLGMDTVLIVIVEDDDSAIIPCRITTDPTPTVTLHNSGVWVPSYDSROGFG 180  
Db 121 VPDPDVAFVPLGMDTVLIVIVEDDDSAIIPCRITTDPTPTVTLHNSGVWVPSYDSROGFG 180  
QY 181 TPTVGYIICEATVKGKKFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
Db 181 TPTVGYIICEATVKGKKFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
QY 241 EVDLQWTPGEGVKGITMLEEIKVPSIKLVYTLVPEATVKDGDYCAARQATREVX 300  
Db 241 EVDLQWTPGEGVKGITMLEEIKVPSIKLVYTLVPEATVKDGDYCAARQATREVX 300  
QY 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVKHFVVEVRAVPPPRISMLKNNLTLENL 360  
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHVKHFVVEVRAVPPPRISMLKNNLTLENL 360  
QY 361 TEITTDVEKIQIRYRSKULIRAKEEDSGHTIIVAQNEADAVKSYTFELLTQVPSILD 420  
Db 361 TEITTDVEKIQIRYRSKULIRAKEEDSGHTIIVAQNEADAVKSYTFELLTQVPSILD 420  
QY 421 VDDHGSTGQTVRCVTCAGTLPDIEMWICKDKKCNNTSWTILANNYSNIITEHSRD 480  
Db 421 VDDHGSTGQTVRCVTCAGTLPDIEMWICKDKKCNNTSWTILANNYSNIITEHSRD 480  
QY 481 RSTVEGRVTFKVEETIYVRCVLAENRELKLVAPTLRSELTVAAAVLLVIVII 540  
Db 481 RSTVEGRVTFKVEETIYVRCVLAENRELKLVAPTLRSELTVAAAVLLVIVII 540  
QY 541 SLIVLVIIWKQPRYIRWRVIESIPDGHYIYVDPMLPYDSRWEFFRDLGLVLRGLG 600  
Db 541 SLIVLVIIWKQPRYIRWRVIESIPDGHYIYVDPMLPYDSRWEFFRDLGLVLRGLG 600  
QY 601 SGAFKVVETAYGLRSQPMKAVKMLKPTARSSEKQALMSELKIMTHLGHPLNIVNL 660  
Db 601 SGAFKVVETAYGLRSQPMKAVKMLKPTARSSEKQALMSELKIMTHLGHPLNIVNL 660  
QY 661 LGACTKSGPIYIITEYCFYGDVLYLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
Db 661 LGACTKSGPIYIITEYCFYGDVLYLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
QY 721 VILSFENNGDYMCKQADTTQYVPMLEKEVSKYDIQRSLYDRPASYYKKSMLDSEVKX 780  
Db 721 VILSFENNGDYMCKQADTTQYVPMLEKEVSKYDIQRSLYDRPASYYKKSMLDSEVKX 780  
QY 781 LLSDDNSEGLTLLDLISFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840  
Db 781 LLSDDNSEGLTLLDLISFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKIVKICDFGLA 840

QY 841 RDIMDSNVYSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900  
DB 841 RDIMDSNVYSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900  
QY 901 VDSFTFNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSPFYHLSEIVENLLPGQYKK 960  
DB 901 VDSFTFNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSPFYHLSEIVENLLPGQYKK 960  
QY 961 SYEKIHLDFLKSDHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
DB 961 SYEKIHLDFLKSDHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
QY 1021 PLPDIIDPVPEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMDDIGIDS 1080  
DB 1021 PLPDIIDPVPEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMDDIGIDS 1080  
QY 1081 SOLVEDSFL 1089  
DB 1081 SOLVEDSFL 1089

RESULT 5

US-08-461-917-2  
; Sequence 2, Application US/08461917  
; Patent No. 6372438  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, Lewis T.  
; APPLICANT: ESCOBEDO, Jaime A.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market, Steuart Street Tower, 20th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,917  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/309,322  
; FILING DATE: 10-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/151,414  
; FILING DATE: 02-FEB-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 2307K-267-2-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/326-2400  
; TELEFAX: 415/326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1089 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-461-917-2  
Query Match 100.0%; Score 5652; DB 3; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPAFVLVGLCLTGLSLILCQLSLPILPNEKVKVQLNSPFLRCFGESEVSWQYP 60  
|||||

DB 1 MGTSPAFVLVGLCLTGLSLILCQLSLPILPNEKVKVQLNSPFLRCFGESEVSWQYP 60  
QY 61 MSEESESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYIY 120  
DB 61 MSEESESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYIY 120  
QY 121 VPDPVAFVPLGMDYLVIVEDDDSGAIIPCRITDPTPTVLHNSGVVPASVDSROGPN 180  
DB 121 VPDPVAFVPLGMDYLVIVEDDDSGAIIPCRITDPTPTVLHNSGVVPASVDSROGPN 180  
QY 181 TTVGPGYICEATVKGKGFOTIPNVYALKATSELDLEMEALKTVYKSGETIVVTVCAVFN 240  
DB 181 TTVGPGYICEATVKGKGFOTIPNVYALKATSELDLEMEALKTVYKSGETIVVTVCAVFN 240  
QY 241 EYVDLQWTPYGEVKGKGIITMBEIEIKVPSIKLVYTLTVPEATVKDSDGYDECAARQATREVK 300  
DB 241 EYVDLQWTPYGEVKGKGIITMBEIEIKVPSIKLVYTLTVPEATVKDSDGYDECAARQATREVK 300  
QY 301 EMKVTISVHEKGFIEIKPTFSQLBAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLENL 360  
DB 301 EMKVTISVHEKGFIEIKPTFSQLBAVNLHEVKHFVVEVRAVPPPRISWLKNNLTLENL 360  
QY 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEADAVKSYTFELLTQVPSIIDL 420  
DB 361 TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEADAVKSYTFELLTQVPSIIDL 420  
QY 421 VDDHGSTGGQTVRCCTAEGTPLPDIEWMICDKIKCNETSWTILANNYSNIITEHSRD 480  
DB 421 VDDHGSTGGQTVRCCTAEGTPLPDIEWMICDKIKCNETSWTILANNYSNIITEHSRD 480  
QY 481 RSTVEGRVTFKVEETIAVRCIAKLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540  
DB 481 RSTVEGRVTFKVEETIAVRCIAKLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540  
QY 541 SLIVLVIIWKQPRYEIRWRVIESIPDGHXYIYVDPMLPYDSRWEFPRDGLVLRVLG 600  
DB 541 SLIVLVIIWKQPRYEIRWRVIESIPDGHXYIYVDPMLPYDSRWEFPRDGLVLRVLG 600  
QY 601 SGAFKVGVEGTAYGLSRQPMKVAVKMLKPTARSSEKQALMSKIMTHLGLPHLAINVL 660  
DB 601 SGAFKVGVEGTAYGLSRQPMKVAVKMLKPTARSSEKQALMSKIMTHLGLPHLAINVL 660  
QY 661 LGACTKSGPIYIITEYCFYGDLYVNLHKNRDSFLSHHPEKPKKELDI FGLNPADESTSY 720  
DB 661 LGACTKSGPIYIITEYCFYGDLYVNLHKNRDSFLSHHPEKPKKELDI FGLNPADESTSY 720  
QY 721 VILSPENNGDYMDKQADTTQVPMLEKVEVSKYSDIQRSLYDRPASYKKKMLDSEVKN 780  
DB 721 VILSPENNGDYMDKQADTTQVPMLEKVEVSKYSDIQRSLYDRPASYKKKMLDSEVKN 780  
QY 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
DB 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
QY 841 RDIMDSNVYSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900  
DB 841 RDIMDSNVYSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM 900  
QY 901 VDSFTFNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSPFYHLSEIVENLLPGQYKK 960  
DB 901 VDSFTFNKIKSGYRMAKPDHATSEVYEIMVKWCNSEPEKRPSPFYHLSEIVENLLPGQYKK 960  
QY 961 SYEKIHLDFLKSDHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
DB 961 SYEKIHLDFLKSDHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
QY 1021 PLPDIIDPVPEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMDDIGIDS 1080  
DB 1021 PLPDIIDPVPEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMDDIGIDS 1080  
QY 1081 SOLVEDSFL 1089  
DB 1081 SOLVEDSFL 1089

## RESULT 6

US-08-464-436-2  
 ; Sequence 2, Application US/08464436  
 ; Patent No. 6514723  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILLIAMS, Lewis T.  
 ; APPLICANT: ESCOBEDO, Jaime A.  
 ; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Crew  
 ; STREET: One Market, Steuart Street Tower, 20th Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/464,436  
 ; FILING DATE: 05-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/309,322  
 ; FILING DATE: 10-FEB-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/151,414  
 ; FILING DATE: 02-FEB-1988  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dow, Karen B.  
 ; REGISTRATION NUMBER: 29,684  
 ; REFERENCE/DOCKET NUMBER: 2307K-267-2-3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/326-2400  
 ; TELEFAX: 415/326-2422  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1089 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-464-436-2

Query Match 100.0%; Score 5652; DB 4; Length 1089;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGTSHPAFLVGLGCLLTGLSLILCOLSLPLPNEKVVQLNSFSRLRCFGESEVSWQYP	60
DB	1	MGTSHPAFLVGLGCLLTGLSLILCOLSLPLPNEKVVQLNSFSRLRCFGESEVSWQYP	60
QY	61	MSEESSDVEIRNEENNSGLFVTLEVSASSAAHTGLTYCYNHTOTENELEGRHIYIY	120
DB	61	MSEESSDVEIRNEENNSGLFVTLEVSASSAAHTGLTYCYNHTOTENELEGRHIYIY	120
QY	121	VDPDVAFLVGLMTDYLIVEDDDSAIIPCRTPDPTVTLNHNSEGVPASVDSRQGFNG	180
DB	121	VDPDVAFLVGLMTDYLIVEDDDSAIIPCRTPDPTVTLNHNSEGVPASVDSRQGFNG	180
QY	181	TFTVGPIYICATVKGKFKOTIPNNVYALKATSELDLEMEALKTVYKSGTIVVTCVFN	240
DB	181	TFTVGPIYICATVKGKFKOTIPNNVYALKATSELDLEMEALKTVYKSGTIVVTCVFN	240
QY	241	EVVDLQWTVFGEVKGKGIWLEIKVPSIKLVYTLVPEATVKDSGDYECARQATREVK	300
DB	241	EVVDLQWTVFGEVKGKGIWLEIKVPSIKLVYTLVPEATVKDSGDYECARQATREVK	300
QY	301	EMKKVTISVHEKGFIEIKPTFSOLEAVNLHEVKHFVVEVRAVPPPRISWLNKNTLIENL	360

DB	301	EMKKVTISVHEKGFIEIKPTFSOLEAVNLHEVKHFVVEVRAVPPPRISWLNKNTLIENL	360
QY	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
DB	361	TEITTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
QY	421	VDDHGSTGQTVRCCTAEGTPLPDIEWMICKDIIKCNNETSWTILANNVSNIIITEHSRD	480
DB	421	VDDHGSTGQTVRCCTAEGTPLPDIEWMICKDIIKCNNETSWTILANNVSNIIITEHSRD	480
QY	481	RSTVEGRVTFKVEETIAVRCLAKNLGAENRELKLVAPTLRSELTVAAAVLVLLVII	540
DB	481	RSTVEGRVTFKVEETIAVRCLAKNLGAENRELKLVAPTLRSELTVAAAVLVLLVII	540
QY	541	SLILVVIWQKQPRYRIRVRVIESISPDGHEIYYVDPMLPYDSRWEFFRDLGLVRVLG	600
DB	541	SLILVVIWQKQPRYRIRVRVIESISPDGHEIYYVDPMLPYDSRWEFFRDLGLVRVLG	600
QY	601	SGAFKVVREGTAYGLRSOPVMKVAVKMLKPTARSEKQALMSELKIMTHLGHPLINVL	660
DB	601	SGAFKVVREGTAYGLRSOPVMKVAVKMLKPTARSEKQALMSELKIMTHLGHPLINVL	660
QY	661	LGACTKSGPIYIITEYCFYGDVNLVHLKNRDGFSLSHHPEKPKKELDI FGLNPADESTRSY	720
DB	661	LGACTKSGPIYIITEYCFYGDVNLVHLKNRDGFSLSHHPEKPKKELDI FGLNPADESTRSY	720
QY	721	VILSFENNGDYMDMKQADTTQVPMLEKVEVSKYSDIQSLYDRPASYKKKSLDSEVK	780
DB	721	VILSFENNGDYMDMKQADTTQVPMLEKVEVSKYSDIQSLYDRPASYKKKSLDSEVK	780
QY	781	LLSDNNSGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
DB	781	LLSDNNSGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA	840
QY	841	RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM	900
DB	841	RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGMM	900
QY	901	VDSFYNKIKSGYRMAKPDHATSEVYEMVKWNSPEKRPSPFYHLSEIVENLLPGQYKK	960
DB	901	VDSFYNKIKSGYRMAKPDHATSEVYEMVKWNSPEKRPSPFYHLSEIVENLLPGQYKK	960
QY	961	SYEKIHLDFLKSHPAVARMVRVDSNAYIGVTYKNEEDKLKDWEGGLDQRLSADSGYII	1020
DB	961	SYEKIHLDFLKSHPAVARMVRVDSNAYIGVTYKNEEDKLKDWEGGLDQRLSADSGYII	1020
QY	1021	PLPDIDVPPEEDLGHNRHSSQTSSESAIETGSSSSTFIKREDETIEDIMMDDIGIDS	1080
DB	1021	PLPDIDVPPEEDLGHNRHSSQTSSESAIETGSSSSTFIKREDETIEDIMMDDIGIDS	1080
QY	1081	SDLVEDSFL 1089	
DB	1081	SDLVEDSFL 1089	

RESULT 7  
 US-08-464-436-2  
 ; Sequence 2, Application US/08464436  
 ; Patent No. 6642022  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILLIAMS, Lewis T.  
 ; APPLICANT: ESCOBEDO, Jaime A.  
 ; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Crew  
 ; STREET: One Market, Steuart Street Tower, 20th Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/464,436  
FILING DATE: 05-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/309,322  
FILING DATE: 10-FEB-1989  
APPLICATION NUMBER: US 07/151,414  
FILING DATE: 02-FEB-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 237K-267-2-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/326-2400  
TELEFAX: 415/326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1090 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-08-464-436-2

Query Match 100.0%; Score 5652; DB 4; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVGLCLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60  
DB 1 MGTSHPAFLVGLCLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60  
QY 61 MSEESESSDVEIRNEENNSGLFTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYIY 120  
DB 61 MSEESESSDVEIRNEENNSGLFTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYIY 120  
QY 121 VPDPPVAFVPLGMDYLVIVVEDDSSAIIIPCRITDPTPTVTLNSEGVPASVDSRQGFNG 180  
DB 121 VPDPPVAFVPLGMDYLVIVVEDDSSAIIIPCRITDPTPTVTLNSEGVPASVDSRQGFNG 180  
QY 181 TTTVGPYICEATVKGKKFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
DB 181 TTTVGPYICEATVKGKKFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
QY 241 EVVDLQWTPYGVKGGITMLBEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREYK 300  
DB 241 EVVDLQWTPYGVKGGITMLBEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREYK 300  
QY 301 EMKKVTISVHEKGFIEIKFTFQSOLEAVNLHVKHFVVEVRAYPPPRISMLKNLTLIENL 360  
DB 301 EMKKVTISVHEKGFIEIKFTFQSOLEAVNLHVKHFVVEVRAYPPPRISMLKNLTLIENL 360  
QY 361 TBITDVEKIQIRYRSKLIKRAKEEDSGHYTIVAQNEADVKSFTFELLTQVPSSILD 420  
DB 361 TBITDVEKIQIRYRSKLIKRAKEEDSGHYTIVAQNEADVKSFTFELLTQVPSSILD 420  
QY 421 VDDHGSTGGQVTRCTAEGTPTPDIEWMCKDIKKNNETSTILANNVSNITTEIHSRD 480  
DB 421 VDDHGSTGGQVTRCTAEGTPTPDIEWMCKDIKKNNETSTILANNVSNITTEIHSRD 480  
QY 481 RSTVEGRVTFKVEETIAVCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540  
DB 481 RSTVEGRVTFKVEETIAVCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540  
QY 541 SLIVLVIIWKQPRYRIRRVIESIPDGHEIYIYDPMQLPYDSRWEFFRDLGLVLRVLG 600  
DB 541 SLIVLVIIWKQPRYRIRRVIESIPDGHEIYIYDPMQLPYDSRWEFFRDLGLVLRVLG 600

QY 601 SGAFKGVVEGTAYGLSRSPQVMKVAVKMLKPTARSSEKQALMSELKIMTHLGHPLNIVNL 660  
DB 601 SGAFKGVVEGTAYGLSRSPQVMKVAVKMLKPTARSSEKQALMSELKIMTHLGHPLNIVNL 660  
QY 661 LGACTKSGPIYIITEYCFYGDVLYNHLKVRDGFSLSHHPEKPKKELDI FGLNPADESTRSY 720  
DB 661 LGACTKSGPIYIITEYCFYGDVLYNHLKVRDGFSLSHHPEKPKKELDI FGLNPADESTRSY 720  
QY 721 VILSPENNGDYMDMKQADTTQVPMLEKKEVSKYSDIQRSLYDRPASYYKKKSMLDSEVKN 780  
DB 721 VILSPENNGDYMDMKQADTTQVPMLEKKEVSKYSDIQRSLYDRPASYYKKKSMLDSEVKN 780  
QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
DB 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
QY 841 RDIHDSNVYKSGSTFLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTTPPGMM 900  
DB 841 RDIHDSNVYKSGSTFLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTTPPGMM 900  
QY 901 VDSTFVNIKSGYRMAKPDHATSEVVEIMVKWNSPEKRPSPFYHLSEIVENLLPQYKK 960  
DB 901 VDSTFVNIKSGYRMAKPDHATSEVVEIMVKWNSPEKRPSPFYHLSEIVENLLPQYKK 960  
QY 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTVYKNEEDKLKOWEGGLDEQRLSADSGYII 1020  
DB 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTVYKNEEDKLKOWEGGLDEQRLSADSGYII 1020  
QY 1021 PLPDDIDPVEEEDLGRNHRSSQTSESAIETGSSSTIKREDETIEDIDMDDIGIDS 1080  
DB 1021 PLPDDIDPVEEEDLGRNHRSSQTSESAIETGSSSTIKREDETIEDIDMDDIGIDS 1080  
QY 1081 SDLVEDSFL 1089  
DB 1081 SDLVEDSFL 1089

RESULT 8

US-09-769-987-2  
; Sequence 2, Application US/09769987  
; Patent No. 6660488  
; GENERAL INFORMATION:  
; APPLICANT: Matsui, Toshimitsu  
; APPLICANT: Aaronson, Stuart A.  
; APPLICANT: Pierce, Jacalyn H.  
; TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor  
; FILE REFERENCE: 14014.0266U2  
; CURRENT APPLICATION NUMBER: US/09/769,987  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 08/460,656  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: US 08/439,095  
; PRIOR FILING DATE: 1995-05-11  
; PRIOR APPLICATION NUMBER: US 07/915,884  
; PRIOR FILING DATE: 1992-07-20  
; PRIOR APPLICATION NUMBER: US 07/308,282  
; PRIOR FILING DATE: 1989-02-09  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1089  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; No. 6660488e =  
; OTHER INFORMATION: synthetic construct  
US-09-769-987-2

Query Match 100.0%; Score 5652; DB 4; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGTSHPAFLVGLCLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60

Db 1 MGTSHPAFLVGLCLTGLSLILCOLSLPILPNEKVVQLNSFSLSRCFGESEVSQWYP 60  
QY 61 MSEEESDVIEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNNHTQTEENELEGRHIYIY 120  
Db 61 MSEEESDVIEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNNHTQTEENELEGRHIYIY 120  
QY 121 VDPDPVAFPLGWTDLVLTVEDDSDAIIPCRITDPTPTVTLHNSGVWVPSVDSRQGFNG 180  
Db 121 VDPDPVAFPLGWTDLVLTVEDDSDAIIPCRITDPTPTVTLHNSGVWVPSVDSRQGFNG 180  
QY 181 TFTVGYICEATVKGKGFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
Db 181 TFTVGYICEATVKGKGFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
QY 241 EVVDLQWTPYGEVKGKGTMLBEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300  
Db 241 EVVDLQWTPYGEVKGKGTMLBEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300  
QY 301 EMKKTIVTSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTILENL 360  
Db 301 EMKKTIVTSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTILENL 360  
QY 361 TEITDVEKIQEIRYRSKULIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420  
Db 361 TEITDVEKIQEIRYRSKULIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420  
QY 421 VDDHGSTGGTQVRCCTAEGTPLPDIEWMICKDKKCNNETSWTILANNYSNIITEHSRD 480  
Db 421 VDDHGSTGGTQVRCCTAEGTPLPDIEWMICKDKKCNNETSWTILANNYSNIITEHSRD 480  
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540  
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540  
QY 541 SLIVLVIWQKPRYRIRWRVIESIPDGHEIYIYDPMQLPYDSRWEFFRDGLVLRGLG 600  
Db 541 SLIVLVIWQKPRYRIRWRVIESIPDGHEIYIYDPMQLPYDSRWEFFRDGLVLRGLG 600  
QY 601 SGAFGKVVEGTAYGLSRQPMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNLVNL 660  
Db 601 SGAFGKVVEGTAYGLSRQPMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNLVNL 660

Db 1081 SDLVEDSFL 1089  
RESULT 9  
US-09-866-510-2  
; Sequence 2, Application US/09866510  
; Patent No. 6667173  
; GENERAL INFORMATION:  
; APPLICANT: KAZLAUSKAS, ANDRIUS  
; APPLICANT: IKUNO, YASUSHI  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES  
; FILE REFERENCE: ERM-104.01  
; CURRENT APPLICATION NUMBER: US/09/866,510  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/250,747  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 60/289,103  
; PRIOR FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1089  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-866-510-2  
Query Match 100.0%; Score 5652; DB 4; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGTSHPAFLVGLCLTGLSLILCOLSLPILPNEKVVQLNSFSLSRCFGESEVSQWYP 60  
Db 1 MGTSHPAFLVGLCLTGLSLILCOLSLPILPNEKVVQLNSFSLSRCFGESEVSQWYP 60  
QY 61 MSEEESDVIEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNNHTQTEENELEGRHIYIY 120  
Db 61 MSEEESDVIEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNNHTQTEENELEGRHIYIY 120  
QY 121 VDPDPVAFPLGWTDLVLTVEDDSDAIIPCRITDPTPTVTLHNSGVWVPSVDSRQGFNG 180  
Db 121 VDPDPVAFPLGWTDLVLTVEDDSDAIIPCRITDPTPTVTLHNSGVWVPSVDSRQGFNG 180  
QY 181 TFTVGYICEATVKGKGFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
Db 181 TFTVGYICEATVKGKGFOTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
QY 241 EVVDLQWTPYGEVKGKGTMLBEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300  
Db 241 EVVDLQWTPYGEVKGKGTMLBEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300  
QY 301 EMKKTIVTSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTILENL 360  
Db 301 EMKKTIVTSVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTILENL 360  
QY 361 TEITDVEKIQEIRYRSKULIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420  
Db 361 TEITDVEKIQEIRYRSKULIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420  
QY 421 VDDHGSTGGTQVRCCTAEGTPLPDIEWMICKDKKCNNETSWTILANNYSNIITEHSRD 480  
Db 421 VDDHGSTGGTQVRCCTAEGTPLPDIEWMICKDKKCNNETSWTILANNYSNIITEHSRD 480  
QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540  
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540  
QY 541 SLIVLVIWQKPRYRIRWRVIESIPDGHEIYIYDPMQLPYDSRWEFFRDGLVLRGLG 600  
Db 541 SLIVLVIWQKPRYRIRWRVIESIPDGHEIYIYDPMQLPYDSRWEFFRDGLVLRGLG 600  
QY 601 SGAFGKVVEGTAYGLSRQPMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNLVNL 660  
Db 601 SGAFGKVVEGTAYGLSRQPMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNLVNL 660

661 LGACTKSGPIYIIITEYCFYGDVNLVHLKQRDSFLSHHPKPKKELDI FGLNPADESTSY 720  
 661 LGACTKSGPIYIIITEYCFYGDVNLVHLKQRDSFLSHHPKPKKELDI FGLNPADESTSY 720  
 721 VILSPENNGDYMCKQADTTQYVPMLEKEVSKYDIQSLYDRPASYKKKSMLDSEVKN 780  
 721 VILSPENNGDYMCKQADTTQYVPMLEKEVSKYDIQSLYDRPASYKKKSMLDSEVKN 780  
 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNVCVHRDLAARNVLLAQQKI VKICDFGLA 840  
 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNVCVHRDLAARNVLLAQQKI VKICDFGLA 840  
 841 RDIMHDSNVSKGSTPLPVKNMAPEISFDNLVLTSLDVMSYGILLWEIFSLGGTTPYGNM 900  
 841 RDIMHDSNVSKGSTPLPVKNMAPEISFDNLVLTSLDVMSYGILLWEIFSLGGTTPYGNM 900  
 901 VDSFTFNKIKSGYRMKPDHATSEVYEIMVKWNSPEKRPSPFYHLSEIVENLLPGQYKK 960  
 901 VDSFTFNKIKSGYRMKPDHATSEVYEIMVKWNSPEKRPSPFYHLSEIVENLLPGQYKK 960  
 961 SYEKIHLDFLKSDDHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020  
 961 SYEKIHLDFLKSDDHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020  
 1021 PLPDDIPVPEEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMDDIGIDS 1080  
 1021 PLPDDIPVPEEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMDDIGIDS 1080  
 1081 SDLVDSFL 1089  
 1081 SDLVDSFL 1089  
 RESULT 10  
 US-09-919-497-90  
 ; Sequence 90, Application US/09919497  
 ; Patent No. 6773883  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mutter, George L.  
 ; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER  
 ; FILE REFERENCE: B0801/7225  
 ; CURRENT APPLICATION NUMBER: US/09/919,497  
 ; CURRENT FILING DATE: 2001-07-31  
 ; PRIOR APPLICATION NUMBER: US 60/221,735  
 ; PRIOR FILING DATE: 2000-07-31  
 ; NUMBER OF SEQ ID NOS: 100  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 90  
 ; LENGTH: 1089  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-919-497-90  
 Query Match 100.0%; Score 5652; DB 4; Length 1089;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MGTSHPAFLVLCGLLTGLSLILCOLSLPILPNEKVKVOLNSSFSLRCFGESEVSNQYP 60  
 1 MGTSHPAFLVLCGLLTGLSLILCOLSLPILPNEKVKVOLNSSFSLRCFGESEVSNQYP 60  
 61 MSEEESDVEIRNEENNSGLFVTLVSVSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120  
 61 MSEEESDVEIRNEENNSGLFVTLVSVSASAAHTGLTYCYNHTQTEENLEGRHIYIY 120  
 121 VPDPPVAFVPLGMDYLVIVVEDDSDAIIFCRITDPTPTVTLHNSGVFPASVDSRQFNG 180  
 121 VPDPPVAFVPLGMDYLVIVVEDDSDAIIFCRITDPTPTVTLHNSGVFPASVDSRQFNG 180  
 181 TPTVGPYICEATVKGKFKQTPIPNVVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240  
 181 TPTVGPYICEATVKGKFKQTPIPNVVALKATSELDLEMEALKTVYKSGETIVVTCVFN 240

241 EVVDLQWTPYGEVKGKGIITMLBEIKVPSIKLVYTLTPVBEATVKDSGDYDECAARQATREV 300  
 241 EVVDLQWTPYGEVKGKGIITMLBEIKVPSIKLVYTLTPVBEATVKDSGDYDECAARQATREV 300  
 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPTPRISMLKNNLTIIENL 360  
 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPTPRISMLKNNLTIIENL 360  
 361 TEITTDVEKIQEIRYRSKLKLRKEEDSGHTYIIVAONEDAVKSYTFELLTQVPSIIDL 420  
 361 TEITTDVEKIQEIRYRSKLKLRKEEDSGHTYIIVAONEDAVKSYTFELLTQVPSIIDL 420  
 421 VDDHSGTGGQVRCRTAEGTPLPDIEWMI CKDIKKCNNETSWTILANNVSNII TEIHSRD 480  
 421 VDDHSGTGGQVRCRTAEGTPLPDIEWMI CKDIKKCNNETSWTILANNVSNII TEIHSRD 480  
 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLSRSELTVAAAVLLVIVII 540  
 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLSRSELTVAAAVLLVIVII 540  
 541 SLIVLVIIWKQPRYEIRWRVIESIPDGHEVYIYVDPMLPYDSRWEFFPRDGLVGRVLG 600  
 541 SLIVLVIIWKQPRYEIRWRVIESIPDGHEVYIYVDPMLPYDSRWEFFPRDGLVGRVLG 600  
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 601 SGAFKGVVGTAYGLSRSQPVKMAVVKMLKPTARSSSEKQALMSELKIMTHLGPLHINVL 660  
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 721 VILSPENNGDYMCKQADTTQYVPMLEKEVSKYDIQSLYDRPASYKKKSMLDSEVKN 780  
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 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNVCVHRDLAARNVLLAQQKI VKICDFGLA 840  
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 841 RDIMHDSNVSKGSTPLPVKNMAPEISFDNLVLTSLDVMSYGILLWEIFSLGGTTPYGNM 900  
 841 RDIMHDSNVSKGSTPLPVKNMAPEISFDNLVLTSLDVMSYGILLWEIFSLGGTTPYGNM 900  
 901 VDSFTFNKIKSGYRMKPDHATSEVYEIMVKWNSPEKRPSPFYHLSEIVENLLPGQYKK 960  
 901 VDSFTFNKIKSGYRMKPDHATSEVYEIMVKWNSPEKRPSPFYHLSEIVENLLPGQYKK 960  
 961 SYEKIHLDFLKSDDHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020  
 961 SYEKIHLDFLKSDDHPAVARMRVDSNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020  
 1021 PLPDDIPVPEEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMDDIGIDS 1080  
 1021 PLPDDIPVPEEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMDDIGIDS 1080  
 1081 SDLVDSFL 1089  
 1081 SDLVDSFL 1089  
 RESULT 11  
 US-09-949-016-6703  
 ; Sequence 6703, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14

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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6703
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6703

Query Match      100.0%; Score 5652; DB 4; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60
DB 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60

QY 61 MSEESESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTCYNNHTQTEENELEGRHIYIY 120
DB 61 MSEESESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTCYNNHTQTEENELEGRHIYIY 120

QY 121 VDDPDVAFVPLGMDTVLIVVEDDSDAIIPCRITDPTPTVTLHNSGVVPASVDSRQGFNG 180
DB 121 VDDPDVAFVPLGMDTVLIVVEDDSDAIIPCRITDPTPTVTLHNSGVVPASVDSRQGFNG 180

QY 181 TETVGPYICEATVKGKFKFTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCAVFN 240
DB 181 TETVGPYICEATVKGKFKFTIPFNVALKATSELDLEMEALKTVYKSGETIVVTCAVFN 240

QY 241 EVVDLOWTPGVEKGIGITMLBEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300
DB 241 EVVDLOWTPGVEKGIGITMLBEIKVPSIKLVYTLTVPEATVKDSDGYECAARQATREVK 300

QY 301 ENKKTVISVHEKGFIBIKFTFQLEAVNLHVKHFVVEVRAYPPPRISMLKNNLTLENL 360
DB 301 ENKKTVISVHEKGFIBIKFTFQLEAVNLHVKHFVVEVRAYPPPRISMLKNNLTLENL 360

QY 361 TRITDVEKIQIRYSKRLKIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420
DB 361 TRITDVEKIQIRYSKRLKIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

QY 421 VDDHGSTGGQVRCVTAEGTLPDIEMWICKIKCNETSTILANNVSNITTEIHSRD 480
DB 421 VDDHGSTGGQVRCVTAEGTLPDIEMWICKIKCNETSTILANNVSNITTEIHSRD 480

QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAALVLLVIVII 540
DB 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAALVLLVIVII 540

QY 541 SLIVLVIIWKQPRYRIRWRVIESIPDGHEIYIYVDPMLPYDSRWEFFPRDGLVLRVLG 600
DB 541 SLIVLVIIWKQPRYRIRWRVIESIPDGHEIYIYVDPMLPYDSRWEFFPRDGLVLRVLG 600

QY 601 SGAFGKVGEGTAYGLSRQPMKVAVKMLKPTARSEKQALMSSELKIMTHLGPLHNLVNL 660
DB 601 SGAFGKVGEGTAYGLSRQPMKVAVKMLKPTARSEKQALMSSELKIMTHLGPLHNLVNL 660

QY 661 LGACTKSGIYIITEYCFYGDVLYLHKNRDGLFSLHHPKPKKELDI FGLNPADESTSY 720
DB 661 LGACTKSGIYIITEYCFYGDVLYLHKNRDGLFSLHHPKPKKELDI FGLNPADESTSY 720

QY 721 VILSPENNGYMDMKQADTQVYVPMLEKVEKYSIDIQRSLYDRPASYKKKMLDSEVKN 780
DB 721 VILSPENNGYMDMKQADTQVYVPMLEKVEKYSIDIQRSLYDRPASYKKKMLDSEVKN 780

QY 781 LLSDDNSEGLTLLDLSFTYVARGNEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840
DB 781 LLSDDNSEGLTLLDLSFTYVARGNEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840

; 841 RDIMHDSNTVSKGSTFLPVKWMAPBSIFDNLVTTLSDVMSYGILLWEIFSLGCTPYPGMM 900
; 841 RDIMHDSNTVSKGSTFLPVKWMAPBSIFDNLVTTLSDVMSYGILLWEIFSLGCTPYPGMM 900
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; 901 VDSFTYFNKIKSGYRMAKPDHATSEVYEIMVKWNSPEKRPFSFYHLSEIVENLLPQYKK 960
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; 1021 PLPDDIDPVEERDLGKRNHSSQTSESAIETGSSSTFIKREDETIEDIMWDDDIGDS 1080
; 1021 PLPDDIDPVEERDLGKRNHSSQTSESAIETGSSSTFIKREDETIEDIMWDDDIGDS 1080
; 1081 SDLVEDSFL 1089
; 1081 SDLVEDSFL 1089

RESULT 12
PCT-US92-00730-4
; Sequence 4, Application PC/TUS9200730
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Stuart Street Tower, 20th Floor \ One Market
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00730
; FILING DATE: 19920128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: 12418-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-00730-4

Query Match      100.0%; Score 5652; DB 5; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60
DB 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60  
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Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYY 120  
QY 121 VPDPAVAFPLGMDTVLIVVEDDDSAIIPCRITDPTPTVTLHNSGVWPASYSRQGFNG 180  
Db 121 VPDPAVAFPLGMDTVLIVVEDDDSAIIPCRITDPTPTVTLHNSGVWPASYSRQGFNG 180  
QY 181 TPTVGPYICATVKGKGFQIIPNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
Db 181 TPTVGPYICATVKGKGFQIIPNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
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Db 241 EVVDLQWTPYGEVKGKGIITMBEIKVPSIKLVYTLTVPEATVKDSDGYECAAARQATREVK 300  
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Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHGVHFFVVEYRAPPRIKNNLTLIENL 360  
QY 361 TEITTOVEKIQEIRYKSKLIRAKEDDSHYTIVAQNEADAVKSYTFELLTQVPSIIDL 420  
Db 361 TEITTOVEKIQEIRYKSKLIRAKEDDSHYTIVAQNEADAVKSYTFELLTQVPSIIDL 420  
QY 421 VDDHGSTGGQVRCVTAEGTLPDIEWMICKKCNNETSWTILANNVSNITIEHSRD 480  
Db 421 VDDHGSTGGQVRCVTAEGTLPDIEWMICKKCNNETSWTILANNVSNITIEHSRD 480  
QY 481 RSTVEGRVTFKVEETIAVCLAKNLLGAENRELKLVAPTIRSELTVAAAVLLVIVII 540  
Db 481 RSTVEGRVTFKVEETIAVCLAKNLLGAENRELKLVAPTIRSELTVAAAVLLVIVII 540  
QY 541 SLILVVIWVKQPRYRIRWVIESIPDGHXYIYVDPMLPYDSRWEPRDGLVLRVLG 600  
Db 541 SLILVVIWVKQPRYRIRWVIESIPDGHXYIYVDPMLPYDSRWEPRDGLVLRVLG 600  
QY 601 SGAFKVGVEGTAYGLSRSPVMKVAVMKLPKPTARSSEKQALMSKIMTHLGHPLINVL 660  
Db 601 SGAFKVGVEGTAYGLSRSPVMKVAVMKLPKPTARSSEKQALMSKIMTHLGHPLINVL 660  
QY 661 LGACTKSGPIIYITEFCYFGLDLYNHLKRDSPSLHHPKPKKELDI FGLNPADESTRY 720  
Db 661 LGACTKSGPIIYITEFCYFGLDLYNHLKRDSPSLHHPKPKKELDI FGLNPADESTRY 720  
QY 721 VILSPENNGDYMDKQADTTQVYVPMLEKRVESKYSDIQSLYDRPASVYKSKMLDSEVKN 780  
Db 721 VILSPENNGDYMDKQADTTQVYVPMLEKRVESKYSDIQSLYDRPASVYKSKMLDSEVKN 780  
QY 781 LLSDDNSEGLTLIDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840  
Db 781 LLSDDNSEGLTLIDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLA 840  
QY 841 RDIMHDSNTVSKGSTPLPKVWMAPEIFDNLYTTLSDVMSYGILLWEIFSLGGTTPYGM 900  
Db 841 RDIMHDSNTVSKGSTPLPKVWMAPEIFDNLYTTLSDVMSYGILLWEIFSLGGTTPYGM 900  
QY 901 VDSFTFNKIKSGYRMAKPDHATSEVYEMVKWNSPEKRPSPHYHSEIVENLLPGQYKK 960  
Db 901 VDSFTFNKIKSGYRMAKPDHATSEVYEMVKWNSPEKRPSPHYHSEIVENLLPGQYKK 960  
QY 961 SYEKIHLDFLKSHPAARMRVDSNAYIGVTYKNEEDKLKOWEGGLDQRLSADSGYII 1020  
Db 961 SYEKIHLDFLKSHPAARMRVDSNAYIGVTYKNEEDKLKOWEGGLDQRLSADSGYII 1020  
QY 1021 PLPDPDPEEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMMDDIGDS 1080  
Db 1021 PLPDPDPEEEDLGKRNHSSQTSSESAIETGSSSSTFIKREDETIEDIMMDDIGDS 1080  
QY 1081 SOLVEDSFL 1089  
Db 1081 SOLVEDSFL 1089

RESULT 13  
PCT-US92-00862-4  
; Sequence 4. Application PC/TUS9200862  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Lewis T.  
; APPLICANT: Escobedo, Jaime A.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND  
; STREET: Steuart Street Tower, 20th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/00862  
; FILING DATE: 19920131  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/151,141  
; FILING DATE: 02-FEB-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/309,322  
; FILING DATE: 10-FEB-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: 2307U-267-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1089 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US92-00862-4

Query Match 100.0%; Score 5652; DB 5; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTEENELEGRHIYY 120  
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Db 121 VPDPAVAFPLGMDTVLIVVEDDDSAIIPCRITDPTPTVTLHNSGVWPASYSRQGFNG 180  
QY 181 TPTVGPYICATVKGKGFQIIPNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
Db 181 TPTVGPYICATVKGKGFQIIPNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
QY 241 EVVDLQWTPYGEVKGKGIITMBEIKVPSIKLVYTLTVPEATVKDSDGYECAAARQATREVK 300  
Db 241 EVVDLQWTPYGEVKGKGIITMBEIKVPSIKLVYTLTVPEATVKDSDGYECAAARQATREVK 300  
QY 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHGVHFFVVEYRAPPRIKNNLTLIENL 360  
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHGVHFFVVEYRAPPRIKNNLTLIENL 360

Db 301 ENKVTISVHEKGFTEIKPTFSQLBAVNLHEVKHFVVEVAYPPPRISMLKNNLTLENL 360  
 QY 361 TEITTDVEKIQRIRSKULIRAKEEDSGHTTIVAQNEADVAKSTFELLTOVPSILDL 420  
 Db 361 TEITTDVEKIQRIRSKULIRAKEEDSGHTTIVAQNEADVAKSTFELLTOVPSILDL 420  
 QY 421 VDDHSGTGQVTRCTAETGTPLPDIEMWICKDKKCNNTSWTILANNVSNITIEHSRD 480  
 Db 421 VDDHSGTGQVTRCTAETGTPLPDIEMWICKDKKCNNTSWTILANNVSNITIEHSRD 480  
 QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAALVLLVIVII 540  
 Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAALVLLVIVII 540  
 QY 541 SLIVLVIWKQPRVEIRNRVIESIPDGHEIYYVDPMLERKEVSKYSDIQRSLYDRPASVKKKMLDSEVKN 600  
 Db 541 SLIVLVIWKQPRVEIRNRVIESIPDGHEIYYVDPMLERKEVSKYSDIQRSLYDRPASVKKKMLDSEVKN 600  
 QY 601 SGAFKGVVEGTAYGLSRSPQVMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNLVNL 660  
 Db 601 SGAFKGVVEGTAYGLSRSPQVMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNLVNL 660  
 QY 661 LGACTKSGPIYIITEYCFYGDVNLVYHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
 Db 661 LGACTKSGPIYIITEYCFYGDVNLVYHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
 QY 721 VILSFENNGDYMDKQADTTQVVPMLERKEVSKYSDIQRSLYDRPASVKKKMLDSEVKN 780  
 Db 721 VILSFENNGDYMDKQADTTQVVPMLERKEVSKYSDIQRSLYDRPASVKKKMLDSEVKN 780  
 QY 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCHRDLAARNVLLAOKIKVICDFGLA 840  
 Db 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCHRDLAARNVLLAOKIKVICDFGLA 840  
 QY 841 RDIMHDSNVKSGSTFLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTTPPGMM 900  
 Db 841 RDIMHDSNVKSGSTFLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTTPPGMM 900  
 QY 901 VDSFTFYNKIKSGYRMAKPDHATSEVVEIMVKCNWSEPEKRPSPFYHLSEIVENLLPQYKK 960  
 Db 901 VDSFTFYNKIKSGYRMAKPDHATSEVVEIMVKCNWSEPEKRPSPFYHLSEIVENLLPQYKK 960  
 QY 961 SYEKIHLDFKSDHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
 Db 961 SYEKIHLDFKSDHPAVARMVDSNAYIGVTYKNEEDKLKDWEGGLDQRLSADSGYII 1020  
 QY 1021 PLPDI DPVEEDLGRNRHSSQTSSESAIETGSSSSTFIKREDETIEDIDMDDIGIDS 1080  
 Db 1021 PLPDI DPVEEDLGRNRHSSQTSSESAIETGSSSSTFIKREDETIEDIDMDDIGIDS 1080  
 QY 1081 SLDVEDSEL 1089  
 Db 1081 SLDVEDSFL 1089

RESULT 14  
 US-09-866-510-10  
 ; Sequence 10, Application US/09866510  
 ; Patent No. 6667173  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KAZLAUSKAS, ANDRIUS  
 ; APPLICANT: IKUNO, YASUSHI  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES  
 ; FILE REFERENCE: ERM-104.01  
 ; CURRENT APPLICATION NUMBER: US/09/866,510  
 ; CURRENT FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: 60/250,747  
 ; PRIOR FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: 60/289,103  
 ; PRIOR FILING DATE: 2001-05-07  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 10

; LENGTH: 1089  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-866-510-10  
 Query Match 99.9%; Score 5649; DB 4; Length 1089;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGTSPAFVLVLCGLTGLSLILCOLSLPILPNEKVVQNLSSPSLRCFCGSESEVSWQYP 60  
 Db 1 MGTSPAFVLVLCGLTGLSLILCOLSLPILPNEKVVQNLSSPSLRCFCGSESEVSWQYP 60  
 QY 61 MSEEBSDDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNNHTQTENELEGRHIYIY 120  
 Db 61 MSEEBSDDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNNHTQTENELEGRHIYIY 120  
 QY 121 VDDPDAVFPVGMTDYLVIVEDDDSAIIPCRTRDTPETPTVTLHNSGVVPASVDSRQGFNG 180  
 Db 121 VDDPDAVFPVGMTDYLVIVEDDDSAIIPCRTRDTPETPTVTLHNSGVVPASVDSRQGFNG 180  
 QY 181 TPTVGPYICEATVKGKFKQTIPFNVYALKATSELEMEALKTVYKSGETIIVTCAVFN 240  
 Db 181 TPTVGPYICEATVKGKFKQTIPFNVYALKATSELEMEALKTVYKSGETIIVTCAVFN 240  
 QY 241 EYVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300  
 Db 241 EYVDLQWTPYGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVK 300  
 QY 301 EMKVTISVHEKGFTEIKPTFSQLBAVNLHEVKHFVVEVAYPPPRISMLKNNLTLENL 360  
 Db 301 EMKVTISVHEKGFTEIKPTFSQLBAVNLHEVKHFVVEVAYPPPRISMLKNNLTLENL 360  
 QY 361 TEITTDVEKIQRIRSKULIRAKEEDSGHTTIVAQNEADVAKSTFELLTOVPSILDL 420  
 Db 361 TEITTDVEKIQRIRSKULIRAKEEDSGHTTIVAQNEADVAKSTFELLTOVPSILDL 420  
 QY 421 VDDHSGTGQVTRCTAETGTPLPDIEMWICKDKKCNNTSWTILANNVSNITIEHSRD 480  
 Db 421 VDDHSGTGQVTRCTAETGTPLPDIEMWICKDKKCNNTSWTILANNVSNITIEHSRD 480  
 QY 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAALVLLVIVII 540  
 Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAALVLLVIVII 540  
 QY 541 SLIVLVIWKQPRVEIRNRVIESIPDGHEIYYVDPMLERKEVSKYSDIQRSLYDRPASVKKKMLDSEVKN 600  
 Db 541 SLIVLVIWKQPRVEIRNRVIESIPDGHEIYYVDPMLERKEVSKYSDIQRSLYDRPASVKKKMLDSEVKN 600  
 QY 601 SGAFKGVVEGTAYGLSRSPQVMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNLVNL 660  
 Db 601 SGAFKGVVEGTAYGLSRSPQVMKVAVKMLKPTARSEKQALMSELKIMTHLGPLHNLVNL 660  
 QY 661 LGACTKSGPIYIITEYCFYGDVNLVYHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
 Db 661 LGACTKSGPIYIITEYCFYGDVNLVYHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
 QY 721 VILSFENNGDYMDKQADTTQVVPMLERKEVSKYSDIQRSLYDRPASVKKKMLDSEVKN 780  
 Db 721 VILSFENNGDYMDKQADTTQVVPMLERKEVSKYSDIQRSLYDRPASVKKKMLDSEVKN 780  
 QY 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCHRDLAARNVLLAOKIKVICDFGLA 840  
 Db 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCHRDLAARNVLLAOKIKVICDFGLA 840  
 QY 841 RDIMHDSNVKSGSTFLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTTPPGMM 900  
 Db 841 RDIMHDSNVKSGSTFLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTTPPGMM 900  
 QY 901 VDSFTFYNKIKSGYRMAKPDHATSEVVEIMVKCNWSEPEKRPSPFYHLSEIVENLLPQYKK 960  
 Db 901 VDSFTFYNKIKSGYRMAKPDHATSEVVEIMVKCNWSEPEKRPSPFYHLSEIVENLLPQYKK 960

Qy 961 SYEKIHLDFLKSDHPAARMRVSDNAYIGVTYKNEEDKLKOWEGGLDEORLSADSGYII 1020  
Db 961 SYEKIHLDFLKSDHPAARMRVSDNAYIGVTYKNEEDKLKOWEGGLDEORLSADSGYII 1020  
Qy 1021 PLPDIDPVEEDLGKRNHSSQTSESAIETGSSSTFFIKREDETIEDIMDDDGIDS 1080  
Db 1021 PLPDIDPVEEDLGKRNHSSQTSESAIETGSSSTFFIKREDETIEDIMDDDGIDS 1080  
Qy 1081 SLDVDSFL 1089  
Db 1081 SLDVDSFL 1089  
RESULT 15  
US-08-180-195-36  
; Sequence 36, Application US/08180195  
; Patent No. 5567584  
; GENERAL INFORMATION:  
; APPLICANT: Sledziwski Ph.D., Andrzej Z  
; APPLICANT: Bell, Lillian A.  
; TITLE OF INVENTION: Kindsvogel Ph.D., Wayne R.  
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS  
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE  
; TITLE OF INVENTION: FUSIONS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/180,195  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,510  
; FILING DATE:  
; APPLICATION NUMBER: US 07/146,877  
; FILING DATE: 22-JAN-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/347,291  
; FILING DATE: 02-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki J.D., David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 990008.446C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; TELEFAX: 206-682-6031  
; TELEX: 3723816  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1089 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-180-195-36  
Query Match 99.9%; Score 5648; DB 1; Length 1089;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGTSHPAFLVGLGCLTGLSLILCOLSLPILPNEKVVQLNSSFSLRCFGESEVSWQYP 60  
Db 1 MGTSHPAFLVGLGCLTGLSLILCOLSLPILPNEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy 61 MSEEESDVEIRNEENNNSGLFVTLVSVSASAAHTGLTYCYNHTQTEENELEGRHIYY 120  
Db 61 MSEEESDVEIRNEENNNSGLFVTLVSVSASAAHTGLTYCYNHTQTEENELEGRHIYY 120  
Qy 121 VDDPDVAFVPLGWTDLVIVEDDDSAIIICRTTDPETPTVTLHNSGVVPSYDSROGFNG 180  
Db 121 VDDPDVAFVPLGWTDLVIVEDDDSAIIICRTTDPETPTVTLHNSGVVPSYDSROGFNG 180  
Qy 181 TPTVGPYICBATVKGKKFOTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
Db 181 TPTVGPYICBATVKGKKFOTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCVAFNN 240  
Qy 241 EVDVLQWTPYGEVKGKITMLBEIKVPSIKLVYTLVTPBATVKDSGDYECARQATREVK 300  
Db 241 EVDVLQWTPYGEVKGKITMLBEIKVPSIKLVYTLVTPBATVKDSGDYECARQATREVK 300  
Qy 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISMLKNNLTLENL 360  
Db 301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAVPPPRISMLKNNLTLENL 360  
Qy 361 TEITTDVEKIQEIRYRSKLIKIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420  
Db 361 TEITTDVEKIQEIRYRSKLIKIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSILD 420  
Qy 421 VDDHGSTGGQVRCCTAECTPLDIEWMI CKDIKKCNNETSWTILANNVSNII TEIHSRD 480  
Db 421 VDDHGSTGGQVRCCTAECTPLDIEWMI CKDIKKCNNETSWTILANNVSNII TEIHSRD 480  
Qy 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540  
Db 481 RSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540  
Qy 541 SLIVLVVWQKPRYERIRWRVIESIPDGHEVITYVDPMLPYDSRWEFPRDGLVGRVLG 600  
Db 541 SLIVLVVWQKPRYERIRWRVIESIPDGHEVITYVDPMLPYDSRWEFPRDGLVGRVLG 600  
Qy 601 SGAFKGVVEGTAYGLSRQPMKAVKMLKPTARSSEKQALMSSELKIMTHLGPLHINVL 660  
Db 601 SGAFKGVVEGTAYGLSRQPMKAVKMLKPTARSSEKQALMSSELKIMTHLGPLHINVL 660  
Qy 661 LGACTKSGPIYIITEYCFYGDVLYLHKNRDPSFLSHHPEKPKKELDI FGLNPADESTSY 720  
Db 661 LGACTKSGPIYIITEYCFYGDVLYLHKNRDPSFLSHHPEKPKKELDI FGLNPADESTSY 720  
Qy 721 VILSPENNGDYMDKQADTTQVVPMLERKEVSKYSDIQSLYDRPASYKKSMLDSEVK 780  
Db 721 VILSPENNGDYMDKQADTTQVVPMLERKEVSKYSDIQSLYDRPASYKKSMLDSEVK 780  
Qy 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
Db 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
Qy 841 RDIMHDSNTVSKGSTFLPVKWMAPESI FDNLYTLTSDVMSYGILLWEI FSLGCTPYGMM 900  
Db 841 RDIMHDSNTVSKGSTFLPVKWMAPESI FDNLYTLTSDVMSYGILLWEI FSLGCTPYGMM 900  
Qy 901 VDSFTFNKIKSGYRMKPDHATSEVYEMVKWNSPEKRPSPFYHLSEVENLLPQYKK 960  
Db 901 VDSFTFNKIKSGYRMKPDHATSEVYEMVKWNSPEKRPSPFYHLSEVENLLPQYKK 960  
Qy 961 SYEKIHLDFLKSDHPAARMRVSDNAYIGVTYKNEEDKLKOWEGGLDEORLSADSGYII 1020  
Db 961 SYEKIHLDFLKSDHPAARMRVSDNAYIGVTYKNEEDKLKOWEGGLDEORLSADSGYII 1020  
Qy 1021 PLPDIDPVEEDLGKRNHSSQTSESAIETGSSSTFFIKREDETIEDIMDDDGIDS 1080  
Db 1021 PLPDIDPVEEDLGKRNHSSQTSESAIETGSSSTFFIKREDETIEDIMDDDGIDS 1080  
Qy 1081 SLDVDSFL 1089  
Db 1081 SLDVDSFL 1089

Search completed: March 11, 2005, 07:50:27  
Job time : 36.7522 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2005, 07:07:56 ; Search time 33.7367 Seconds  
(without alignments)  
3105.821 Million cell updates/sec

Title: US-10-027-400-2

Perfect score: 5652

Sequence: 1 MGTSHPAFLVGLCLTGLSL.....IDMDDIGDSSDLVEDSFL 1089

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5652	100.0	1089	1 PFHUGA	platelet-derived g
2	5190.5	91.8	1088	1 PFRTGA	platelet-derived g
3	5177	91.6	1089	1 S33727	Platelet-derived g
4	4246	75.1	1087	2 I51552	platelet-derived g
5	2354.5	41.7	1106	1 PFHUGB	platelet-derived g
6	2336.5	41.3	1098	1 PFMSRB	platelet-derived g
7	2182.5	38.6	1048	2 T30815	platelet-derived g
8	1914.5	33.9	457	2 S44269	platelet-derived g
9	1481.5	26.2	977	2 I45877	protein-tyrosine k
10	1461.5	25.9	960	1 JN0677	protein-tyrosine k
11	1458	25.8	976	1 A49814	protein-tyrosine k
12	1454.5	25.7	978	1 TVRHUKT	protein-tyrosine k
13	1446.5	25.6	975	1 TVMSKT	protein-tyrosine k
14	1416.5	25.1	954	2 I51703	C-kit-related kina
15	1412.5	25.0	980	1 TVCTMD	macrophage colony-
16	1400.5	24.8	941	1 TVMVMU	protein-tyrosine k
17	1395	24.7	975	2 T30816	macrophage colony-
18	1352.5	23.9	978	2 T16385	macrophage colony-
19	1346.5	23.8	972	1 TVRHMD	macrophage colony-
20	1344	23.8	976	1 TVMSMD	macrophage colony-
21	1287	22.8	1338	2 S09882	protein-tyrosine k
22	1280	22.6	1333	2 T78875	receptor tyrosine
23	1278	22.6	1336	2 I60598	Fit-1 tyrosine kin
24	1231.5	21.8	1330	2 S49010	embryonic receptor
25	1226	21.7	1348	2 S51656	vascular endotheli
26	1206.5	21.3	1356	2 JC1402	protein-tyrosine k
27	1198.5	21.2	1379	2 J43954	vascular endotheli
28	1164.5	20.6	1000	2 S18827	Flt3 protein - mou
29	1163.5	20.6	1298	2 A48999	protein-tyrosine k

#### ALIGNMENTS

##### RESULT 1

PFHUGA

platelet-derived growth factor receptor alpha precursor - human

N;Contains: protein-tyrosine kinase (EC 2.7.1.112)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004

C;Accession: A40162; A32941

R;Matsui T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle, W.; Kraus, M.; Pierce, J.

Science 243, 800-804, 1989

A;Title: Isolation of a novel receptor cDNA establishes the existence of two PDGF receptor

A;Reference number: A40162; MUID:89130149; PMID:2536956

A;Accession: A40162

A;Molecule type: mRNA

A;Residues: 1-1089 <MATS>

A;Cross-references: UNIPROT:P16234; GB:M21574; NID:G189733; PIDN:AAA96715.1; PID:G189734

R;Claesson-Welsh, L.; Eriksson, A.; Westermark, B.; Heldin, C.H.

Proc. Natl. Acad. Sci. U.S.A. 86, 4917-4921, 1989

A;Title: cDNA cloning and expression of the human A-type platelet-derived growth factor

A;Reference number: A32941; MUID:89296915; PMID:2544881

A;Accession: A32941

A;Molecule type: mRNA

A;Residues: 1-1089 <CLA>

A;Cross-references: GB:M22734; NID:G189725; PIDN:AAA60048.1; PID:G189726

C;Comment: The extracellular domain is predicted to include five immunoglobulin-like doma

C;Genetics:

A;Gene: GDB:PDGFRA

A;Cross-references: GDB:120267; OMIM:173490

A;Map position: 4q11-4q12

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

C;Keywords: ATP; autophosphorylation; dimer; glycoprotein; growth factor receptor; phosph

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-1089/Product: platelet-derived growth factor receptor alpha #status predicted <MAT>

F;25-524/Domain: extracellular #status predicted <EX>

F;42-102/Domain: immunoglobulin homology <IMM1>

F;143-191/Domain: immunoglobulin homology <IMM2>

F;228-292/Domain: immunoglobulin homology <IMM3>

F;428-503/Domain: immunoglobulin homology <IMM4>

F;525-548/Domain: transmembrane #status predicted <TMW>

F;549-1089/Domain: intracellular #status predicted <INT>

F;591-957/Domain: protein kinase homology <KIN>

F;599-607/Region: protein kinase ATP-binding motif

F;42,76,103,179,353,359,458,468/Binding site: carbohydrate (Asn) (covalent) #status predi

F;49-100,150-189,235-290,435-501/Disulfide bonds: #status predicted

F;627/Active site: Lys #status predicted

F;849/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 100.0%; Score 5652; DB 1; Length 1089;

Best Local Similarity 100.0%; Pred. No. 3.3e-238;

Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVGLCLTGLSLPILPNEKVKVOLNSSFSLRCFGEVSNQYP 60

|||||

Db	1	MGTSHPAFVLVGLCLTGLSLILCQLSLPSILPNEKVKVQLNSFSRLRCFGESEVSNQYP	60
QY	61	MSBEESDVIRNEENNNGSLFVTVLEVSSASAAHTGLTYCYNHTTOTEENELEGRHIYY	120
Db	61	MSBEESDVIRNEENNNGSLFVTVLEVSSASAAHTGLTYCYNHTTOTEENELEGRHIYY	120
QY	121	VPPDPVAFVPLGMDYLVIVEDDSDSAILIPCRITDPTPTVTLHNSGVSPASYSRQGFNG	180
Db	121	VPPDPVAFVPLGMDYLVIVEDDSDSAILIPCRITDPTPTVTLHNSGVSPASYSRQGFNG	180
QY	181	TFTVGPYICBATVKGKKFQIPNNVALKATSELDLEMEALKTVYKSGETIVTTCVAFNN	240
Db	181	TFTVGPYICBATVKGKKFQIPNNVALKATSELDLEMEALKTVYKSGETIVTTCVAFNN	240
QY	241	EVVDLQWTPGVEYKGGIGITWLESIKVPISIKLVVTLTVPEATVKDGDYCAARQATREVK	300
Db	241	EVVDLQWTPGVEYKGGIGITWLESIKVPISIKLVVTLTVPEATVKDGDYCAARQATREVK	300
QY	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISMKNLTLIENL	360
Db	301	EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISMKNLTLIENL	360
QY	361	TEITTDVEKIQEIRYRSKKLIRAKBEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
Db	361	TEITTDVEKIQEIRYRSKKLIRAKBEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD	420
QY	421	VDDHGSTGCGVRCVTAEGTPLPDIEWMICKDIKKCNNTSWTILANNYSNIITEHSRD	480
Db	421	VDDHGSTGCGVRCVTAEGTPLPDIEWMICKDIKKCNNTSWTILANNYSNIITEHSRD	480
QY	481	RSTVEGRVTFPAKVEETIAVRCLAKNLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII	540
Db	481	RSTVEGRVTFPAKVEETIAVRCLAKNLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII	540
QY	541	SLILVVIWIKQPRYRIRNRVIESISPDGHEIYIVDPMQLPYDSRWEFFRDGLVLRGLG	600
Db	541	SLILVVIWIKQPRYRIRNRVIESISPDGHEIYIVDPMQLPYDSRWEFFRDGLVLRGLG	600
QY	601	SGAFGKVEGTAGLRSQPVKMAVKMLKPTARSSEKQALMSSELKIMTHLGHPLMIVNL	660
Db	601	SGAFGKVEGTAGLRSQPVKMAVKMLKPTARSSEKQALMSSELKIMTHLGHPLMIVNL	660
QY	661	LGACTKSGPIYIITEYCFYGDVLYNLHKRDSFLSHHPEKPKKELDI FGLNPADESTRSY	720
Db	661	LGACTKSGPIYIITEYCFYGDVLYNLHKRDSFLSHHPEKPKKELDI FGLNPADESTRSY	720
QY	721	VILSFENNNGDYMCKQADTTQYVPMLEKEVSKYSDIQSLYDRPASYYKKSMLDSEVKN	780
Db	721	VILSFENNNGDYMCKQADTTQYVPMLEKEVSKYSDIQSLYDRPASYYKKSMLDSEVKN	780
QY	781	LLSDDNSEGLTLDLISFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDPGLA	840
Db	781	LLSDDNSEGLTLDLISFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDPGLA	840
QY	841	RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTLTSDVMSYGILLWEIFSLGCTPYPGMM	900
Db	841	RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTLTSDVMSYGILLWEIFSLGCTPYPGMM	900
QY	901	VDSTFYNKIKSGYRMAKPDHATSEVVEIMVKCNWSEPEKRPSPYHLSEIVENILLPQYKK	960
Db	901	VDSTFYNKIKSGYRMAKPDHATSEVVEIMVKCNWSEPEKRPSPYHLSEIVENILLPQYKK	960
QY	961	SYEKIHLDFLKSHPAVARMRVSDNAYIGVTTYKNEEDKLKDWEGGLDQORLSADSGYII	1020
Db	961	SYEKIHLDFLKSHPAVARMRVSDNAYIGVTTYKNEEDKLKDWEGGLDQORLSADSGYII	1020
QY	1021	PLPDIDPVPPEEDLGRNHRSSQTSBESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS	1080
Db	1021	PLPDIDPVPPEEDLGRNHRSSQTSBESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS	1080
QY	1081	SDLVDSFL 1089	
Db	1081	SDLVDSFL 1089	

RESULT 2

PFTGA

platelet-derived growth factor receptor alpha precursor - rat  
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text\_change 09-Jul-2004  
A;Accession: A34710; S33767; S25100  
R;Lee, K.H.; Bowen-Pope, D.F.; Reed, R.R.  
Mol. Cell. Biol. 10, 2237-2246, 1990  
A;Title: Isolation and characterization of the alpha platelet-derived growth factor receptor  
A;Reference number: A34710; MUID:90220609; PMID:2157969  
A;Accession: A34710  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1088 <LE>  
A;Cross-references: UNIPROT:P20786; GB:M63837; NID:G202929; PIDN:AAA0743.1; PID:G202930  
A;Note: in the authors' translation an additional residue, Val, is shown after position 1  
R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.  
Biochim. Biophys. Acta 1173, 294-302, 1993  
A;Title: Conservation in sequence and affinity of human and rodent PDGF ligands and receptor  
A;Reference number: S33764; MUID:93305723; PMID:8318539  
A;Accession: S33767  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 33-149, 'R', 151-518, 'T', 520-523 <HER1>  
A;Cross-references: EMBL:Z14118; NID:G56863; PIDN:CAA78488.1; PID:G56864  
R;Experimental source: strain Sprague Dawley  
R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.  
submitted to the EMBL Data Library, July 1992  
A;Description: Cross-species conservation in sequence and function of PDGF ligands and receptor  
A;Reference number: S25096  
A;Accession: S25100  
A;Molecule type: mRNA  
A;Residues: 33-149, 'R', 151-518, 'T', 520-523 <HER2>  
A;Cross-references: EMBL:Z14118; NID:G56863; PIDN:CAA78488.1; PID:G56864  
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
C;Keywords: ATP; autophosphorylation; glycoprotein; heterodimer; homodimer; phosphoprotein;  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-1088/Product: platelet-derived growth factor receptor alpha #status predicted <MAT>  
F;24-523/Domain: extracellular #status predicted <EXT>  
F;41-101/Domain: immunoglobulin homology <IMM1>  
F;142-190/Domain: immunoglobulin homology <IMM2>  
F;227-291/Domain: immunoglobulin homology <IMM3>  
F;427-502/Domain: immunoglobulin homology <IMM4>  
F;524-547/Domain: transmembrane #status predicted <TM>  
F;548-1088/Domain: intracellular #status predicted <INT>  
F;590-956/Domain: protein kinase homology <KIN>  
F;598-606/Region: protein kinase ATP-binding motif  
F;48-99, 149-188, 234-289, 434-500/disulfide bonds: #status predicted  
F;75, 76, 88, 102, 178, 352, 358, 457, 467/binding site: carbohydrate (Asn) (covalent) #status predicted  
F;626/Active site: Lys #status predicted  
F;848/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 91.8%; Score 5190.5; DB 1; Length 1088;  
Best Local Similarity 90.9%; Pred. No. 3.6e-218;  
Matches 990; Conservative 55; Mismatches 43; Indels 1; Gaps 1;

QY	1	MGTSHPAFVLVGLCLTGLSLILCQLSLPSILPNEKVKVQLNSFSRLRCFGESEVSNQYP	60
Db	1	MGTSQ-AFLVLSCLLTGPSLIVCQLLPSILPNEKIVPLSSFSRLRCFGESEVSNQHP	59
QY	61	MSBEESDVIRNEENNNGSLFVTVLEVSSASAAHTGLTYCYNHTTOTEENELEGRHIYY	120
Db	60	MSBEEDPNVIRTEENNNSLFTVLEVNVASAAHTGWTCYCNHTTQTESEIEGRHIYY	119
QY	121	VPPDPVAFVPLGMDYLVIVEDDSDSAILIPCRITDPTPTVTLHNSGVSPASYSRQGFNG	180
Db	120	VPPDPMAFVPLGMDYLVIVEDDSDSAILIPCLITDPTPTVTLHNNGLVSPASYSRQGFNG	179
QY	181	TFTVGPYICBATVKGKKFQIPNNVALKATSELDLEMEALKTVYKSGETIVTTCVAFNN	240

Db 180 TFSVGPYICEATVRGRFTKTSFNVVALKATSELNLEMDTROQTVYKAGETIVVTCVAFNN 239  
QY 241 EVVDLQWTPYGVKGIGITWLEIKVPSIKLVYTLVPEATVKDSDGYECAARQATREVK 300  
Db 240 EVVDLQWTPYGVVRNGITWLEIKVPSIKLVYTLVPEATVKDSDGYECAARQATREVK 299  
QY 301 EMKKTIVTSVHEKGFIEIKTFTFSQLEAVNLHVKHFVVEVRAYPPPRISMKNLTIENL 360  
Db 300 EMKKTIVTSVHEKGFVQIRPTFGHLETVNLHVQREFVVEVQAYPTPRISMKNLTIENL 359  
QY 361 TEITTDVEKIOEIRYRSKLIKIRAKEDSGHYTIVAQEDAVKSYTFELLTQVPSILDL 420  
Db 360 TEITTDVQSRQETRYOSKLIKIRAKEDSGHYTIIIVQNDMDKSYTFELSTLVPASILDL 419  
QY 421 VDDHGSTGGQTVRCATAGTPLPDIEWMIKCKIKKCNNTSWTILANNYSNIITEHSRD 480  
Db 420 VDDHSGGGQTVRCATAGTPLPDIEWMIKCKIKKCNNTSWTILANNYSNIITEHQRG 479  
QY 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540  
Db 480 RSTVEGRVSFAKVEETIAVRCLAKNLLGIGNRELKLVAPLSRSELTVAAAVLLVIVIV 539  
QY 541 SLILVVIWVKQPRYIRWRVIESISPDGHEHYIYVDPMLPYDSRWEFFRDGLVLRVLG 600  
Db 540 SLILVVIWVKQPRYIRWRVIESISPDGHEHYIYVDPMLPYDSRWEFFRDGLVLRVLG 599  
QY 601 SGAFKGVREGTAYGLSRQPMVKVAVKMLKPTARSSEKQALMSELKIMTHLGHPLINVL 660  
Db 600 SGAFKGVREGTAYGLSRQPMVKVAVKMLKPTARSSEKQALMSELKIMTHLGHPLINVL 659  
QY 661 LGACTKSGPIYIITEYCFYGDVNLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
Db 660 LGACTKSGPIYIITEYCFYGDVNLHKNRDSFMSRHEKPKKLDI FGLNPADESTRSY 719  
QY 721 VILSFENNNDYMDKQADTTQYVPMLEKEVSKYSDIQSLYDRPASYYKKSMLDSEVK 780  
Db 720 VILSFENNNDYMDKQADTTQYVPMLEKEVSKYSDIQSLYDRPASYYKKSMLDSEAK 779  
QY 781 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840  
Db 780 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 839  
QY 841 RDIMHDSNVYKSGSTFLPVKMAPEISFDNLYTTLSDVMSYGLLWEIFSLGCTPYPGMM 900  
Db 840 RDIMHDSNVYKSGSTFLPVKMAPEISFDNLYTTLSDVMSYGLLWEIFSLGCTPYPGMM 899  
QY 901 VDSFTFNKIKSGYRMKAPDHATSEVYIMVQWNSPEKRPSPYHLSEIVENLLPGQYK 960  
Db 900 VDSFTFNKIKSGYRMKAPDHATSEVYIMVQWNSPEKRPSPYHLSEIVENLLPGQYK 959  
QY 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNEEDLKQWEGGLDEORLSADSGYII 1020  
Db 960 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNEEDLKQWEGGLDEORLSADSGYII 1019  
QY 1021 PLPDIDPVEEDLGRNHRSSQTSBESAIETGSSSTFIKREDETIEDIDMDDIGIDS 1080  
Db 1020 PLPDIDPVEEDLGRNHRSSQTSBESAIETGSSSTFIKREDETIEDIDMDDIGIDS 1079  
QY 1081 SDLVEDSFL 1089  
Db 1080 SDLVEDSFL 1088

RESULT 3  
S33727  
platelet-derived growth factor receptor alpha precursor - mouse  
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: I57511; S33727  
R;Stiles, C.D.; Wang, C.  
Mol. Cell. Biol. 10, 6781-6784, 1990  
A;Title: Retinoic acid promotes transcription of the platelet-derived growth factor alpha

A;Reference number: I57511; MUID:91061789; PMID:2174116  
A;Accession: I57511  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1089 <RES>  
A;Cross-references: UNIPROT:P26618; GB:M57683; NID:g199783; PIDN:AAA39733.1; PID:g199784  
C;Genetics:  
A;Gene: PDGF-alpha-R  
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
C;Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transmembrane  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;228-292/Domain: immunoglobulin homology <IMM>  
F;591-957/Domain: protein kinase homology <KIN>  
F;599-607/Region: protein kinase ATP-binding motif  
F;42,76,89,103,179,353,359,458,468,506/Binding site: carbohydate (Asn) (covalent) #statu  
Query Match 91.6%; Score 5177; DB 1: Length 1089;  
Best Local Similarity 91.0%; Pred. No. 1.4e-217;  
Matches 991; Conservative 50; Mismatches 48; Indels 0; Gaps 0;  
QY 1 MGTSHPAFLVGLCLLTGLSLILCOLSLPILPNEKVKVQLNSSFSLRCFGESEVSWQVP 60  
Db 1 MGTSHQVFLVLSCLLTGPGLISCOLLPSILPNEKIVQLNSSFSLRCVGESEVSWQHP 60  
QY 61 MSEESESSOIVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYIY 120  
Db 61 MSEEEDPNVEIRSEENNSGLFVTVLEVNVASAAHTGWYTCYNNHTQTDESEIEGRHIYIY 120  
QY 121 VDDPDAVFLPGLTDLVIVVEDDSAIIPCRTTDPETPTLHNSGVNPASVDSROGFG 180  
Db 121 VDDPDAVFLPGLTDLVIVVEDDSAIIPCRTTDPETPTLHNSGVNPASVDSROGFG 180  
QY 181 TPTVGPYICEATVKGKFKOTIPFNVALKATSELNLEMDTROQTVYKAGETIVVTCVAFNN 240  
Db 181 TFSVGPYICEAIVKGTFTKTSFNVVALKATSELNLEMDTROQTVYKAGETIVVTCVAFNN 240  
QY 241 EVVDLQWTPYGVKGIGITWLEIKVPSIKLVYTLVPEATVKDSDGYECAARQATREVK 300  
Db 241 EVVDLQWTPYGVVRNGITWLEIKVPSIKLVYTLVPEATVKDSDGYECAARQATREVK 300  
QY 301 EMKKTIVTSVHEKGFIEIKTFTFSQLEAVNLHVKHFVVEVRAYPPPRISMKNLTIENL 360  
Db 301 EMKKTIVTSVHEKGFIEIKTFTFSQLEAVNLHVKHFVVEVRAYPPPRISMKNLTIENL 360  
QY 361 TEITTDVEKIOEIRYRSKLIKIRAKEDSGHYTIVAQEDAVKSYTFELLTQVPSILDL 420  
Db 361 TEITTDVQSRQETRYOSKLIKIRAKEDSGHYTIIIVQNDMDKSYTFELSTLVPASILDL 420  
QY 421 VDDHGSTGGQTVRCATAGTPLPDIEWMIKCKIKKCNNTSWTILANNYSNIITEHSRD 480  
Db 421 VDDHSGGGQTVRCATAGTPLPDIEWMIKCKIKKCNNTSWTILANNYSNIITELPRRG 480  
QY 481 RSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLLVIVII 540  
Db 481 RSTVEGRVSFAKVEETIAVRCLAKNLLSVVARELKLVAPTLSRSELTVAAAVLLVIVIV 540  
QY 541 SLILVVIWVKQPRYIRWRVIESISPDGHEHYIYVDPMLPYDSRWEFFRDGLVLRVLG 600  
Db 541 SLILVVIWVKQPRYIRWRVIESISPDGHEHYIYVDPMLPYDSRWEFFRDGLVLRVLG 600  
QY 601 SGAFKGVREGTAYGLSRQPMVKVAVKMLKPTARSSEKQALMSELKIMTHLGHPLINVL 660  
Db 601 SGAFKGVREGTAYGLSRQPMVKVAVKMLKPTARSSEKQALMSELKIMTHLGHPLINVL 660  
QY 661 LGACTKSGPIYIITEYCFYGDVNLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY 720  
Db 661 LGACTKSGPIYIITEYCFYGDVNLHKNRDSFMSRHEKPKKLDI FGLNPADESTRSY 720  
QY 721 VILSFENNNDYMDKQADTTQYVPMLEKEVSKYSDIQSLYDRPASYYKKSMLDSEVK 780  
Db 721 VILSFENNNDYMDKQADTTQYVPMLEKEVSKYSDIQSLYDRPASYYKKSMLDSEVK 780  
QY 781 LLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

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Db 781 LLSDDSEGLTLDLSFTYQVARGMEFLASKNCVHRDLAARNVLAQKIVKICDFGLA 840
QY 841 RDIMHSDNYVSKGSTFLPVKWMAPESIFDNLVTTLSDVMSYSGILLWEIFSLGCTPYPGMM 900
Db 841 RDIMHSDNYVSKGSTFLPVKWMAPESIFDNLVTTLSDVMSYSGILLWEIFSLGCTPYPGMM 900
QY 901 VDSFTFNKIKSGYRMKAPDHATSEVVEIMVKCNSEPEKPPSPYHLSSEIVENILLPGQYKK 960
Db 901 VDSFTFNKIKSGYRMKAPDHATSEVVEIMVKCNSEPEKPPSPYHLSSEIVENILLPGQYKK 960
QY 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTKNEEDKLKOWEGGLDEORLSADSGYII 1020
Db 961 SYEKIHLDFLKSHPAVARMRVDSNAYIGVTKNEEDKLKOWEGGLDEORLSADSGYII 1020
QY 1021 PLPDIDPVEEDLGKRNHSSQTSSESAIETGSSSTFIKREDETIEDIMMDDIGIDS 1080
Db 1021 PLPDIDPVEEDLGKRNHSSQTSSESAIETGSSSTFIKREDETIEDIMMDDIGIDS 1080
QY 1081 SDAVEDSFL 1089
Db 1081 SDAVEDSFL 1089

RESULT 4
I51552
platelet-derived growth factor A receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51552
R;Jones, S.D.; Ho, L.; Smith, J.C.; Yordan, C.; Stiles, C.D.; Mercola, M.
Dev. Genet. 14, 185-193, 1993
A;Title: The xenopus platelet-derived growth factor alpha receptor: cDNA cloning and dem
ion.
A;Reference number: I51552; MUID:93365089; PMID:8358864
A;Accession: I51552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1087 <JON>
A;Cross-references: UNIPROT:P26619; GB:M80798; NID:g214652; PIDN:AAA49929.1; PID:g214653
C;Genetics:
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; growth factor receptor
F;43-103/Domain: immunoglobulin homology <IM>
F;593-957/Domain: protein kinase homology <KIN>
F;601-609/Domain: protein kinase ATP-binding motif

Query Match 75.1%; Score 4246; DB 2; Length 1087;
Best Local Similarity 75.6%; Pred. No. 3.8e-177;
Matches 821; Conservative 104; Mismatches 153; Indels 8; Gaps 6;

QY 7 AFLVLGCLL-TGSLILCOLSLPSILPNEKNKVQVNSFLRCFGSEVSWQYPMSEBE 65
Db 7 ASLILGCLLTIIGWAILAENPLFTIPDKDELQALHSSFTLKCTGSEVSWQPNNSPE 66
QY 66 SSDVEIRNEENNSGLFVTVLEVSSAAGTGLTCVYNHTQTEENLEGRHIVVYVDPDP 125
Db 67 KQNVIRSEENNSGLFVSLILEVSDAFAFDGLTCVYNHTQTEENLEGRHIVVYVDPDP 126
QY 126 VAFVPLGMDTLYLVIVDDSDSAIIPCRITDPTETVTLHNSG--VVPASVDSRQFNGTFT 183
Db 127 VPAPFGLFDHIIIVVEDESALVPCRTDPSSEVTLKNISSRTVFAFYDSKQGFAGNFP 186
QY 184 VGYICEATVKGKFKQTPINPVVALKATSELDLEMAKLVYKSGETIVVTCAVFNNEV 243
Db 187 PGSIYICETTSKNMYQTEPYILQTKATHNISVMEAPKTFMFRAGETIADCIVLDNEV 246
QY 244 DLQWTPGVEKVGKGIITMLBEIKVPSIKLVTVTLVPEATVKDSGDYECARQATREVKEM 303
Db 247 DLKWTIPGQGVGIRNVESEKVPYQRLVTLTANATTEDSGEYCAVIHATLDNRVK 306
QY 304 KVTISVHEKGFBIKPTFSQLEAVNLHVKHFVVEVRAYPPPPRISWLKNNLTLIENLTEI 363
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Db 307 KNIIVTHEKGFIDLEPMFGSEFANLHEVKSFIYNLHAYPTGCLFWLKNRNLSENLTET 366
QY 364 TTDVEKIQIRVRSKLIRAKKEPSGHYTVIAQNEADVAKSYTFELLTOVPSIILDLVDD 423
Db 367 TTSIVTTKETRFQSKLIRAKKEPSGLYTLVAQNDRETKSYFIIQIKVPALILELVOK 426
QY 424 HGSSTGGQVTRCTAEGTFLPDJEMWICKDKKCNNETSWTILANNVSNITTEHSRDRST 483
Db 427 HEGASGEQVCLAKGMPVDVWELVCKDKRCNNDTLMSIILATNGSEISMETH-ODDEQ 485
QY 484 VEGRTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVISLI 543
Db 486 IESQVTFKLEETMAIRCIKNELGWVARELKLVAPTLRSELTVAAAVLVLLVIVISLI 545
QY 544 VLVVIWQKPRYEIRWRVIESISPDGHEVYIYDPMOLPYDSRWEPFRDGLVLRVIGSGA 603
Db 546 VLVVIWQKPRYEIRWRVIESISPDGHEVYIYDPMOLPYDSRWEPFRDGLVLRVIGSGA 605
QY 604 FGKVVGEATAYGLSRQPMKAVKMLKPTARSEKQALMSELKIMTHLPHLNLVNLGA 663
Db 606 FGKVVGEAAYGLSRQPMKAVKMLKPTARSEKQALMSELKIMTHLGAHLNLVNLGA 665
QY 664 CTKSGPIYIITBYCFYGDVLYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVIL 723
Db 666 CTKSGPIYIITBYCFYGDVLYLHKNRDNFQSRHPEKPKKOLDIFGLNPADESTRSYVIL 725
QY 724 SFENNGDYMDKQADTTQVPMLEKEVSKYSDIQSLYDRPASYYKKKMLDSEVKNLLS 783
Db 726 SFENNGDYMDKQADTMQVPMLEKPEKSKYSDIQSLYDRPASYYKKKPL--SEVKNILS 783
QY 784 DNSEGLTLDLSFTYQVARGMEFLASKNCVHRDLAARNVLAQKIVKICDFGLARDI 843
Db 784 DQFEGLTVDLDSFTYQVARGMEFLASKNCVHRDLAARNVLAQKIVKICDFGLARDI 843
QY 844 MHDNSVYSGSTFLPVKWMAPESIFDNLVTTLSDVMSYSGILLWEIFSLGCTPYPGMMVDS 903
Db 844 MHDNSVYSGSTFLPVKWMAPESIFDNLVTTLSDVMSYSGILLWEIFSLGCTPYPGMMVDS 903
QY 904 TFYNKIKSGYRMKAPDHATSEVVEIMVKCNSEPEKPPSPYHLSSEIVENILLPGQYKSYE 963
Db 904 TFYNKIKSGYRMKAPDHATSEVVEIMVKCNSEPEKPPSPYHLSSEIVENILLPGQYKSYE 963
QY 964 KTHLDFLKSDHPAVARMRVDSNAYIGVTKNEEDKLKOWEGGLDEORLSADSGYIIPLP 1023
Db 964 TVLHDFLKSDHPAVARMRVDSNAYIGVTKNEH-KMKDREGDFDORLSADSGYIIPLP 1022
QY 1024 DIDPVEEDLGKRNHSSQTSSESAIETGSSSTFIKREDETIEDIMMDDIGIDSSDL 1083
Db 1023 DIDPVEDES-GKRNHSSQTSSESAIETGSSSTFIKRDDETIEDIMMDDIGIDSSDL 1081
QY 1084 VEDSFL 1089
Db 1082 VEDSFL 1087

RESULT 5
PFUGB
platelet-derived growth factor receptor beta precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A28206; A31195; A38268; A31925; B31925; C31925
R;Gronwald, R.G.K.; Grant, F.J.; Haldeman, B.A.; Hart, C.E.; O'Hara, P.J.; Hagen, F.S.; F.
Proc. Natl. Acad. Sci. U.S.A. 85, 3435-3439, 1988
A;Title: Cloning and expression of a cDNA coding for the human platelet-derived growth fa
A;Reference number: A28206; MUID:88217915; PMID:2835772
A;Accession: A28206
A;Molecule type: mRNA
A;Residues: 1-1106 <GRO>
A;Cross-references: UNIPROT:P09619; GB:J03278; NID:g189731; PIDN:AAA60049.1; PID:g189732
R;Claesson-Welsh, L.; Eriksson, A.; Moren, A.; Severinsson, L.; Ek, B.; Cestman, A.; Betu
Mol. Cell. Biol. 8, 3476-3486, 1988
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Nature 323, 226-232, 1986  
A;Title: Structure of the receptor for platelet-derived growth factor helps define a fam  
A;Reference number: A25742; MUID:87014762; PMID:3020426  
A;Accession: A25742  
A;Molecule type: mRNA  
A;Residues: 1-1098 <VAR>  
A;Cross-references: UNIPROT:P05622; EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619  
A;Note: part of this sequence, including the amino end of the mature protein, was confir  
C;Comment: The extracellular domain is predicted to include five immunoglobulin-like dom  
C;Comment: The purified receptor was found to be ubiquitinated.  
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer;  
F;1-31/Domain: signal sequence #status predicted <SIG>  
F;32-1098/Product: platelet-derived growth factor receptor beta #status predicted <MAT>  
F;32-530/Domain: extracellular #status predicted <EXT>  
F;46-101/Domain: immunoglobulin homology <IMM1>  
F;141-191/Domain: immunoglobulin homology <IMM2>  
F;227-292/Domain: immunoglobulin homology <IMM3>  
F;428-509/Domain: immunoglobulin homology <IMM4>  
F;531-554/Domain: transmembrane #status predicted <TM>  
F;555-1098/Domain: intracellular #status predicted <INT>  
F;597-964/Domain: protein kinase homology <KIN>  
F;605-613/Region: protein kinase ATP-binding motif  
F;44,88,102,214,291,306,353,370,444,467,478/Binding site: carboxydrate (Aen) (covalent)  
F;53-99,148-189,234-290,435-507/Disulfide bonds: #status predicted  
F;633/Active site: Lys #status predicted  
F;856/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 41.3%; Score 2336.5; DB 1; Length 1098;  
Best Local Similarity 44.1%; Pred. No. 3.3e-94;  
Matches 498; Conservative 192; Mismatches 356; Indels 83; Gaps 21;

QY 6 PAFLVIG-CLLTGLSLILCOLSLPSIL-PNENKVVQLNSFSLRCFGESEVSWQPMSE 63  
DB 8 PALVLRQQLLSVLVLGTPQTSRGLVITPPEGFVLNLSITFVLTCGSGAPVNM----- 61

QY 64 EESSDVEIRNEE--NNSGLFVTVLEVSSASAAHTGLTYCYNNHTQTENELEGRIHIYVYP 122  
DB 62 EQMSQVPQWQEAANNQDGTFSVLTLLNVTGDTGEVFCVYNNSLGPELS-ERKRIYIFVP 120

QY 123 DPVAVFLGWTYLVIVEDDDSAIIPCRITDPTETVTLNNSGVVP--ASYDSRGGFNG 180  
DB 121 DPTMGFLPMDSDFLIFVTDVTTIPCRVTPDQLEVLTHKKVDIPLHVPYDQHGFTG 180

QY 181 TETVGPVICATYKGGKFFQIPNNVALKATSELDLEMEALKTVYKSGETIVTCAVFN 240  
DB 181 TFDKTYICTTIGDREVDGTYVLSLQVSS--INVSNAVQTVVRQGESITIRCIVMGN 239

QY 241 EVVDLQWTPYGEVKGIGITMLEE--IKVPSIKLVITLTVPEATVKDSGDYECARQATRE 298  
DB 240 DVVNFWQTYPRMKSRLVPEVPTDYLFGVPS-RIGSILHIPTAELSDSGTYTCNVSVSVND 298

QY 299 VKEMKKVTISVHKGFIETKPTSQLAEVNLHVKHFVVEVRAYPPTPRISLWLNKNNLTLE 358  
DB 299 HGDEKAINISVIENGIVYRLLETGLDVEIAELHRSRLTRVVFEEYAPMPSPVLMLKDNRTLGD 358

QY 359 N-LTEITTDVEKIQEIRYRSKLLIRAKEDSGHYITVAQNEIDAVKSYTFELLTQVPSI 417  
DB 359 SGAGELVLRNNSETRYISELLVVRKVEAGYITNRAFDEDEVLQSLQVNVFVRV 418

QY 418 LDLDVDDHGGTGGQVRCRTAEGTFLPDIEWMIKDKIKKNNETSWTLANNVSNITIEH 477  
DB 419 LEL-SESHPANGQOTIRCRGRGMPQPNVTWTSTCRDLKRCPRKLSPTPLGNS----- 468

QY 478 SRDRSTVEGRVTP-----AKVETIAVRCIAKULLGAENRELKLVAPTLR 522  
DB 469 SKESQLENTVTFWEEDQEVYVSTLRLRHVDQPLSVRCMLQNSMGDSQEVTVVPHSLP 528

QY 523 SELTVAALVLLVIVISLVLVWTKQPRYERWRVIESIPDGHEIYVYDPMOLPY 592  
DB 529 FKVVVISAILALVVLVVISLILMLQKPRYERWRVIESVSSDGHEIYVYDPMOLPY 598

QY 583 DSRWEFPRDGLVLRVLGSGAFGKVEGTAYGSRSQPVKMKVAVKMLKPTARSEKQALM 642

DB 589 DSTWELPRQLVLGRLLSGAGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALM 648  
QY 643 SELKIMTHLGPHLNIVNLGACTKSGPIYIITEYCYGLDVLNVLHKNRDSFSLHPEK-- 700  
DB 649 SELKIMSHLGPHLNIVNLGACTKSGPIYIITEYCRYGLDVLNVLHKNRKHFTLQRHSHKHC 708

QY 701 -PKKELDIFGLNAPADSTSYVTLSPENNGDYMDKQADTTQVPMLEKREKYSYSDIOR 759  
DB 709 PPSAEIYSNAL-PVGFSLPSHLNLTGESDGGYNDMSKDESIDYVPMLEMDKGDIKYADIES 767

QY 760 SLYDRPASYYKKSMLESDVKNLSDNSRGLTLLDLSFTYQVARGWFEFLASNCVHRDL 819  
DB 768 PSYMAFYDNYVSPAPRTYATLIND-SPVLSYTDLVGFSYQVANGMDFLASNCVHRDL 826

QY 820 AARNVLLAOGKIVKICDFGLARDIMHDSNYVSGSTFLPVKWMAPESIFDNLVTTLSDVW 879  
DB 827 AARNVLICGKLVKICDFGLARDIMRDSNYISKGSTYFLPVKWMAPESIFNSLYTTLSDVW 886

QY 880 SYGILLWEIPLSGGTPEYPCGMVDSFTYKIKSGYRMAKPDHATSEVVEYIMVKWCNSEPEK 939  
DB 887 SFGILLWEIPLSGGTPEYPCGMVDSFTYKIKSGYRMAKPDHATSEVVEYIMVKWCNSEPEK 946

QY 940 RPSFYHLSIVENLLPQGYKYSYEKTHLDLFXSDHPAVARMR-----VDSNA 987  
DB 947 RPPFSQVLLERLLGEGYKYYQVDFEFLRSDHPAILRSQARFPGIHLRSLPLDTSSV 1006

QY 988 YGVTVYNEEDKLKDWEGGLDQRSLDSAGYIIPDIDPVPEEDL--GKNRHSQSOTS 1045  
DB 1007 LYTAVQFNE-----SDNDYIIPDPKPDVADGLPGSPSLASSTLN 1049

QY 1045 EESAITGSSSTFIKRED-----ETIEDIDMDDDIGDSS-DLVEDSFL 1089  
DB 1050 EVNTSITICDPLQLQEPQAPAEQLEQDSCGCPGLAEADSFL 1098

RESULT 7  
T30815  
platelet-derived growth factor receptor beta - Japanese pufferfish  
C;Species: Fugu rubripes (Japanese pufferfish)  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: T30815  
R;How, G.F.; Venkatesh, B.; Brenner, S.  
Genome Res. 6, 1185-1191, 1996  
A;Title: Conserved linkage between the pufferfish (Fugu rubripes) and human genes for plat  
A;Reference number: Z20882, MUID:97129405; PMID:89733913  
A;Accession: T30815  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1048 <HOW>  
A;Cross-references: UNIPROT:P79749; EMBL:U63926; NID:gl752706; PID:gl752707; PIDN:AAC6006  
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

Query Match 38.6%; Score 2182.5; DB 2; Length 1048;  
Best Local Similarity 43.9%; Pred. No. 1.5e-87;  
Matches 472; Conservative 175; Mismatches 334; Indels 93; Gaps 25;

QY 9 LVLGCLLTGLSLILCOLSLPSILPNENKVVQLNSFSLRCFGESEVSWQ-----YPM 61  
DB 16 VALAALLSCTTVSCL-----KIVPEEKQLILAEGLSLSLTCAGSSETTDLKSDDDVFFQ 71

QY 62 SEESDSDVIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNNHTQTENELEGRIHIYV 121  
DB 72 MKAESDNLNKKVQNS--TASVLTILWHVDWKNATVYQC-----REQLTGEIKVAVFV 123

QY 122 PPDVAVFLGPM-----TDVLNIVVEDDDSAIIPCRITDPTETVTLNNSGVVPAS--YDSR 175  
DB 124 PD---RFSQTLRFIESSHGVTKTSGESVTPCVVTPNITVTLYDKDTLDPVNGVYVPS 180

QY 176 QGFNGCTFTVGPYICATVKGKFFQIPNNVALKATSELDLEMEALKTVYKSGETIVTWC 235  
DB 181 EGFKAYLDVRYTCRGLNGEVKESQAFNVYSIHVHPEDIDAYVNASQTVLKGQEPLTVNC 240





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Db      130  NDTLVRCLTDPETVNTSLTGCES-KELPKDL-----TFVADPKAGITIRNVKREVHRL 182
Qy      189  ---CEATVKGKQTTPFNV---YALKATSELEMEALKTVY--KSGETIVVTCVAFN- 239
Db      183  CLHCSANQRGKSLSKFTLKVRAAIKAVPVWSVS-----KTSYLLREGBEFAVTCLIKDV 238
Qy      240  NEVVLDQWTPGVEKGGIITMLBEEKVPSIKLV--YTLTVPEATVKDSGDYECAARQATR 297
Db      239  SSVSDSMWIKENSQQTKAQTKKNSWQGDPSYLRQERLTIS SARVNDSGVFMCIYANNFTG 298
Qy      298  EVKEMKKVTISVHKEGFIEIKTFPSQLEAVNLHEVHFVVEVAYPPP-RISMLKNNLT 356
Db      299  SAN--VTTILEVVDKGFINFPMWNTTVFVNDGENVDLVVEYAYPKPVHRQWIYNNRTS 356
Qy      357  IENLTETDVEKIQIRYRSKULKIRAKEEDSGHYTIYAQNEDAVKSYTFELLTQVPS 416
Db      357  TDKWDYPKS-ENESNIRYVNLHLRLKGTGEGTYTFHVSNDVNSSVTFNYYVNTKPE 415
Qy      417  ILDLVDDHGSTGGQVRCRTAEGTLPDLEWMIKDI-KKCNNETSWTILANNVSNITTE 475
Db      416  ILT-----HDLVNGMLQCVAAFPPEPTIDWYFCPGTEGRCSVP-----VGPVDVQ 461
Qy      476  IHSRDRSTVEGRVTFPAKVEETI-----AVRCLAKNLLGAE-----NRELKLVAPT 520
Db      462  IQNSSVSPFGKLVYSTIDDSYTFKHNGTVBCRAYNDVGKSSASFNAFKGNSKEQIHAHT 521
Qy      521  LRSELVAAAVLVLVIVISLVIVVWVKQPRYIRWRVETISIPDGHGYIYVDPMLQ 580
Db      522  LFTPLLIGFVIAAGLCMFY--MLTYKYLQKPMYEQVMKWBEI--NGNNYYVIDPTQL 577
Qy      581  PYDSRWEFRDGLVGLRGVSGAFGKVEGTAYGLSRQPMKVAVKMLKPTARSSEKOA 640
Db      578  PYDKHKEFPNRRLSFGKTLGAGAFGKVEATAYGLKSDAAMTVAVKMLKPSAHLTEREA 637
Qy      641  LMSCLKIMTHLPHLNVNLLGACTSGPIYIITEYCFYGDLYVNLHKNRDPSFLSHPEK 700
Db      638  LMSCLKVLSYGLNHMNVNLLGACTIGGPTLVITEYCCYGDLLNLRKRDRDSCFKSQED 697
Qy      701  PKELDI FGLNPADESTRSVILSFPENGDYMDMKQADTQYVPMLEKEVSKYDIQRS 760
Db      698  HAEVALYKNLLHSKESCN-----DSTNEYMDMPG--VSYY-----VPTKADKRS 742
Qy      761  LYDRPASYYKKMSLMDSEVNKLSDDNSEGLTLDDLSTFYQVARGMEFLASKNCVHRDLA 820
Db      743  A--RIGSY-----IERDVTPEIMEDDELALDLELLSFSYQVAKNAFLASKNCIHRDLA 795
Qy      821  ARNVLLAQGVKIKICDFGLARDIMHDSNVYSKSGSTFLPVKWMAPESIFDNLYTTLSDVWS 880
Db      796  ARNILLTHGRITKICDFGLARDIKDINSYVYVGNARLPVKWMAPEISFNCVYTFESDVWS 855
Qy      881  YGILLWEIFSLGTPYPGMWVDSFTFYKIKSGYRMAKPDHATSEVYEIMVKWCNSPEKR 940
Db      856  YGIFLWELFSLGSPYPGMPVDSFKFYKMKEGFRMLSPHEHAPAEYDIDMKTCWDADPLKR 915
Qy      941  PSFYHLSEIVENLLPGQYKKSKYKIHLDLFKSDHPAVAL--MRVDS 984
Db      916  PTFKQIVOLIEKQISESTNHIYNSLANCSPHRENPAVDHSVRINS 960

RESULT 10
JN0677
protein-tyrosine kinase (EC 2.7.1.12), receptor type kit precursor - chicken
N:Alternate names: tyrosine kinase receptor kit
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JN0677
R:Sasaki, E.; Okamura, H.; Chikamune, T.; Kanai, Y.; Watanabe, M.; Naito, M.; Sakurai, M.
Gene 128, 257-261, 1993
A:Title: Cloning and expression of the chicken c-kit proto-oncogene.
A:Reference number: JN0677; MUID:9322995; PMID:7685729
A:Accession: JN0677
A:Molecule type: mRNA
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A:Residues: 1-960 <SAS>
A:Cross-references: UNIPROT:Q08156; DDBJ:D13225; NID:G303532; PIDN:BA02506.1; PID:G30353
A:Experimental source: brain
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
rotein kinase
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-960/Product: tyrosine kinase receptor #status predicted <MAT>
F:314-380/Domain: immunoglobulin homology <IMM>
F:573-916/Domain: protein kinase homology <KIN>
F:581-589/Region: protein kinase ATP-binding motif
F:76,135,149,269,286,318,338,356,453,469/Binding site: carbohydrate (Asn) (covalent)

Query Match      25.9%; Score 1461.5; DB 1; Length 960;
Best Local Similarity 36.1%; Pred. No. 2.9e-56;
Matches 365; Conservative 148; Mismatches 359; Indels 139; Gaps 30;

Qy      1  MGTSPAFVLVGLCLTGLSLILCQLSLPSILPNEKENVVQLNSFSRLRCFGESEVSWQYP 60
Db      1  MEGAHLAWELAHAVLL-LSLIPAGSVPH--EESLVLVNGKEBLRLKCNESGPVTWNF- 55
Qy      61  MBEESDVEIRNEENNSGLFTVLEVSASAAHTGLTYCYNNHTOTENELEG----RHI 117
Db      56  QNSDPSAKTRISNEKE-----WHTKNATIRDIGRYEC-----KSGSTVNSF 97
Qy      118  YIVVDPDVAFVPLGMDYLVIVEDDDSAIIPCRITDDET-PVTLHNSG-VVPASYDSR 175
Db      98  YFVKDQPNVLF-----LVDSLIVGKSDSLILVCPLTDPVLNFTLRKCDGKPLK- 148
Qy      176  QGFNGTFTVGP-----YICEATVKG--KKFQTIIPNVVAL-KATSELDL 216
Db      149  ---NMTFIPNPQGIIRKVNQVSFKGYCQLAKHNGVEKISEHIFLNVRPVHKALPVITL 205
Qy      217  EMEALKTVYKSETIVVTCVAFNNEVDLQWTPVEYKGGKITMLEEIKVPSIKLV- 272
Db      206  SKS--YELLKEGEEFEVTCIITD---VD-----SSVKASWISYKSAIVTSKRNLDGYG 254
Qy      273  ---YTLTVPEATVKDSGDYECAARQATREVEMKKTIVISVHEKGFIEIKPTFSQLEAVN 328
Db      255  YERKLTNIRSVGVNDSGEFTQCAENPFG--KTNATVTLKALAKGFVRLFATWNTIDIN 312
Qy      329  LHEVHFVVEVAYPPPRIS-WLKNKNTLTIENLTETDVEKIQIRYRSKULIRAKBE 387
Db      313  AQONGNLTVYEAYPKPEEVVMWYNETL-QNSDHYVVKFTVGNNSYTSSELHLRLKGT 371
Qy      388  DSGHTIVVAQNEDAVKSYTFELLTQVPSILDLVDDHGSTGGQVRCRTAEGTLPDIEW 447
Db      372  EGGIYTFVFSNSDASSVTFNYYVTKPBEILTL-----DMLGNDILQCVATGFPAPTIV 426
Qy      448  MICKDI-KKCNNETSWTILANNVSNITTEIHSRDRSTVEGRVTFPAKVEETIARVCLAKNL 506
Db      427  YFCPGTEQRCLDSPITSPMDVKVSYTNSVSPSFERILVESTVNASMFKSTGTICCEA--- 483
Qy      507  LGAENRELKLV-----APTLRSELVAAAVLVLLVIVISLVIVLWVIMVKQKPY 555
Db      484  --SSNGDKSSVFPNFAIKEQIRHTLFTPLLAFAAGLMCIIV--MTLVIVYLQKPY 539
Qy      556  EIRWRVIESIPDGHGYIYVDPMLQPYDSRWEFRDGLVGLRGVSGAFGKVEGTAYGL 615
Db      540  EVQWKVVEEI--NGNNYVIDPTQPYDHKEWFPNRRLSFGKTLGAGAFGKVEATAYGL 597
Qy      616  SRSQPMKVAVVXKMLKPTARSSEKQALMSKELKIMTHLPHLNTVNLGACTSGPIYITE 675
Db      598  FKSDAAMTVAVKMLKPSAHLTEREALMSKELKVLSGYLNHINIVNLLGACTIGGPTLVITE 657
Qy      676  YCFYGDLYVNLHKNRDSEI-----SHPEKPKELDIFGLNPADESTRSVILSPENGDY 731
Db      658  YCYGDLNLFNLRKRKDSFTCPKHEEHAEAAVYENLLHQAEPTADAV-----NEY 706
Qy      732  MDMKQADTQYVPMLEKEVSKYSDIQRSLYDRPASYYKKKMSLMDSEVNKLLSDDNSEGLT 791
Db      707  MDMKPGVSVAVPPKADKK-----RPV--KSGSYTDQDVTLSMLEDDDELALD 750
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Qy 792 LLLDLSFTYQVARGMFLASKNVHRDLAARNVLLAQQKIVTKICDFGLARDIMHDSNYVS 851  
 Db 751 VEDLLSFSYQVARGMFLASKNVHRDLAARNVLLAQQKIVTKICDFGLARDIRDSNYVV 810  
 Qy 852 KGSTFLPVKWMAPESIFDNLVLTSLDWSVSGILLWELFSLGSGTPYPCMMVDSSTFYNNKIS 911  
 Db 811 KGNARLPVKWMAPESIFDNLVLTSLDWSVSGILLWELFSLGSGTPYPCMMVDSSTFYNNKIR 870  
 Qy 912 GYRMAKPDHATSVEYIWMKMNSEPEKPSFVHLGSLVENLLPGQYKKS 962  
 Db 871 GYRMPSECPPEMYDIMKSCWADPLQRTFFQIQLVIEQQLSDNAPRY 921  
 RESULT 11  
 A49814  
 protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: A49814; S49088  
 R:Tsujimura, T.; Hirota, S.; Nomura, S.; Niwa, Y.; Yamazaki, M.; Tono, T.; Morii, E.; Kitajima, T.; Tono, T.; Yamazaki, M.; Nomura, S.; Kitamura, Y.  
 Blood 78, 1942-1946, 1991  
 A:Title: Characterization of Ws mutant allele of rats: a 12-base deletion in tyrosine kinase  
 A:Reference number: A49814; MUID:92003944; PMID:1912577  
 A:Accession: A49814  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-978 <TSU>  
 A:Cross-references: UNIPROT:Q63116; GB:D12524; NID:9220707; PIDN:BAA02094.1; PID:9220708  
 R:Tsujimura, T.; Tono, T.; Yamazaki, M.; Nomura, S.; Kitamura, Y.  
 submitted to the EMBL Data Library, October 1991  
 A:Description: Two isoforms of rat c-kit receptor tyrosine kinase.  
 A:Reference number: S49088  
 A:Accession: S49088  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-511,516-978 <TS2>  
 A:Cross-references: EMBL:X62491; NID:9509135; PIDN:CAA44354.1; PID:9509136  
 C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
 C:Keywords: ATP; autophosphorylation; phosphotransferase; tyrosine-specific protein kinase  
 F:129-188/Domain: immunoglobulin homology <IMM>  
 F:589-932/Domain: protein kinase homology <KIN>  
 F:597-605/Region: protein kinase ATP-binding motif

Db 347 HQOMIYNNRT-PTNRGDEVKSDNQSNIRYVNBRLRLTRLKGTEGGYTYFLVNSDVSASV 405  
 Qy 406 TFBELLTQVPSIIIDLVDHGGSTGGQTVRCRTABGTPLPDIEMMICKDKIKKNNETSWTIL 465  
 Db 406 TFDVYNTTPEILLTYDLNMG-----RLQCVAAAGFPETIDWYFC-----TGAEQRCV- 454  
 Qy 466 ANVSNIIITEIHSRRDSTVEGRVTFPAKVEETI-----AVRCLAKNLLGAE----- 510  
 Db 455 --PVPDQVQIQNASVSPFGKLVQSSIDSSVFRHNGTVECKASNAVKGSAFFNFPAFKG 512  
 Qy 511 NRELKLVAPTLRSELVAAAVLLVLIISLVLVIMKQKPRYELRWVIESISPDGH 570  
 Db 513 NSKEIQPHLTFPLLLIGFVVTAGLIGIIV--MVLAYKYLQKPEYEVQMKVSEI--NGN 568  
 Qy 571 EYIYDPMQLPYDSRWEPFRDGLVLGRVLGSGAFGKVECTAYGLSRSQPMVKVAVKMLK 630  
 Db 569 NYVYIDTQLPYDHKWEFPNRNLSFGKTLGAGAFGVVEATAYGLIKSDAAMTVAVKMLK 628  
 Qy 631 PTARSEKQALMSKELMTHLGHPLNIVNLLGACTSGPIIYITEYCFYGDVLVNYLHNR 690  
 Db 629 PSAHLTEREALMSKELVSLYGLNHNINVLGACTVGGPTLVITEYCCYGDLLNLFRRKR 688  
 Qy 691 DSFLSHHPKPKKELDIFGLNPADESTRSVILSFENNGDYMDKQADTTQYVPMLEKE 750  
 Db 689 DSFIFSKBEQADAALYKNLLHSKES-----SCDSSNEYMDMKPG-VSYVVP----- 734  
 Qy 751 VSKYSDIQRLSDRPAKYKKKMLDSEVKNLLSDNDEGLTLLDLSFTYQVARGMEFLA 810  
 Db 735 -----TKTKRSARISDIYERDVTPTAIMEDELDLDELDSFSQVAKGMAFLA 785  
 Qy 811 SKNCVHRDLAARNVLLAQQKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDN 870  
 Db 786 SKNCIHRDLAARNVLLTHGRITKICDFGLARDIRDSNYVVKGNARLPVKWMAPESIFNC 845  
 Qy 871 LYTLLSDWSYGILLWEISLGGTPYPCMMVDSSTFYNNKISGYRMAKPDHATSVEYIWM 930  
 Db 846 VYTFEDVWSYGIFFLWELFSLGSGTPYPCMMVDSSTFYNNKISGYRMAKPDHATSVEYIWM 905  
 Qy 931 KCWNSPEKRPSPHYLSEIVENLLPGQYKKSYSKIHLDLFLKSDHPAVA--RMRVDS 984  
 Db 906 TCWDADPLKRPFPKQVQVLIIEKQISDSSKHIYNLANCNPENPVVDHSVRVNS 961  
 RESULT 12  
 TVHUKT  
 protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - human  
 N:Alternate names: mast/stem cell growth factor receptor; tyrosine kinase receptor c-kit  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text\_change 09-Jul-2004  
 C:Accession: S01426; A41815; A41815; B41815; C41815; I37948; I56954; I54336  
 R:Yarden, Y.; Kuang, W.J.; Yang-Feng, T.; Coussens, L.; Munemitsu, S.; Dull, T.J.; Chen, EBO J. 6, 3341-3351, 1987  
 A:Title: Human proto-oncogene c-kit: a new cell surface receptor tyrosine kinase for an  
 A:Reference number: S01426; MUID:88111521; PMID:2448137  
 A:Accession: S01426  
 A:Molecule type: mRNA  
 A:Residues: 1-976 <YAR>  
 A:Cross-references: UNIPROT:P10721; GB:X06182; NID:934084; PIDN:CAA29548.1; PID:934085  
 R:Hu, W.X.; Cornu, F.; Andre, C.; Galibert, F.  
 Chinese Biochem. J. 7, 618-629, 1991  
 A:Title: Nucleotide sequence of two neighbouring fragments of human c-kit proto-oncogene  
 A:Reference number: PC1015  
 A:Accession: PC1015  
 A:Molecule type: DNA  
 A:Residues: 412-713 <HUM>  
 A>Note: article in Chinese with English abstract  
 R:Spritz, R.A.; Giebel, L.B.; Holmes, S.A.  
 Am. J. Hum. Genet. 50, 261-269, 1992  
 A:Title: Dominant negative and loss of function mutations of the c-kit (mast/stem cell g  
 A:Reference number: A41815; MUID:92133600; PMID:1370874  
 A:Accession: A41815  
 A:Molecule type: DNA  
 A:Residues: 579-583,'L',585-589 <SPR>

A:Cross-references: GB:S78839; NID:G244084; PIDN:AAB21234.1; PID:G244085  
A>Note: sequence extracted from NCBI backbone (NCBIN:78839, NCBI:P:78842)  
A>Note: disease-related mutant from patient with piebaldism  
A:Accession: B41815  
A:Molecule type: DNA  
A:Residues: 637-641, 'SPELPW' <SP2>  
A:Cross-references: GB:S78843; NID:G244086; PIDN:AAB21235.1; PID:G244087  
A>Note: sequence extracted from NCBI backbone (NCBIN:78843, NCBI:P:78844)  
A>Note: disease-related mutant from patient with piebaldism  
A:Accession: C41815  
A:Molecule type: DNA  
A:Residues: 556-560, 'GGDKWK' <SP3>  
A:Cross-references: GB:S78845; NID:G244088; PIDN:AAB21236.1; PID:G244089  
A>Note: sequence extracted from NCBI backbone (NCBIN:78845, NCBI:P:78846)  
A>Note: disease-related mutant from patient with piebaldism  
R:Giebel, L.B.; Strunk, K.M.; Holmes, S.A.; Spritz, R.A.  
Oncogene 7, 2207-2217, 1992  
A:Title: Organization and nucleotide sequence of the human KIT (mast/stem cell growth factor receptor) proto-oncogene.  
A:Reference number: I56954; MUID:94103107; PMID:7506248  
A:Accession: I56954  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-22 <RE2>  
A:Cross-references: GB:S67773; NID:G459358; PIDN:AAB29529.1; PID:G459359  
R:Spritz, R.A.; Holmes, S.A.; Berg, S.Z.; Nordlund, J.J.; Fukai, K.  
Hum. Mol. Genet. 2, 1499-1500, 1993  
A:Title: A recurrent deletion in the KIT (mast/stem cell growth factor receptor) proto-oncogene.  
A:Reference number: I54336; MUID:94061059; PMID:7694728  
A:Accession: I54336  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 242-250 <RE3>  
A:Cross-references: GB:S67686; NID:G460545; PIDN:AAD13996.1; PID:G4261696  
C:Genetics:  
A:Gene: GDB:KIT  
A:Cross-references: GDB:I20117; OMIM:164920  
A:Map position: 4q12-4q12  
A:Introns: 23/1; 113/1; 207/1; 252/3; 309/1; 372/2; 411/1; 449/2; 514/1; 549/3; 592/1; 601/1  
A>Note: defects in this gene may result in piebaldism  
C:Function:  
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP  
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; kinase-related protein; tyrosine-specific protein kinase  
F:1-976/Product: protein-tyrosine kinase kit precursor, long form #status predicted <MAT>  
F:1-509,514-976/Product: protein-tyrosine kinase kit precursor, short form #status predicted <MAT>  
F:1-22/Domain: signal sequence #status predicted <Sig>  
F:23-976/Product: protein-tyrosine kinase kit #status predicted <MAT>  
F:23-520/Domain: extracellular #status predicted <EXT>  
F:51-99/Domain: immunoglobulin homology <IMM1>  
F:129-188/Domain: immunoglobulin homology <IMM2>  
F:226-292/Domain: immunoglobulin homology <IMM3>  
F:328-394/Domain: immunoglobulin homology <IMM4>  
F:423-493/Domain: immunoglobulin homology <IMM5>  
F:521-543/Domain: transmembrane #status predicted <TMN>  
F:544-976/Domain: intracellular #status predicted <INT>  
F:587-931/Domain: protein kinase homology <KIN>  
F:595-603/Region: protein kinase ATP-binding motif  
F:58-97,136-186,233-290,428-493/Disulfide bonds: #status predicted  
F:130,145,283,293,300,320,352,367,463,486/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:623,640,792/Active site: Lys, Glu, Asp #status predicted  
F:797,810/Binding site: magnesium (Asn, Asp) #status predicted

Query Match	25.7%	Score 1454.5	DB 1	Length 976
Best Local Similarity	35.7%	Pred. No. 5.9e-36		
Matches 352	Conservative 150	Mismatches 356	Indels 129	Gaps 26
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DB	35	SPPSIHFGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE-----TNEKNQENWIT--	84	
QY	86	EVSASAAHTGLYTCYNYHTOTTENELEGRHIIYIYVDPDPAVFVPLGMDTYLVIVEDDS	145	
DB	85	--EKAETATNGKYTCTNKHGLSNS-----IYFVRDPAKLF--LVDRLYSGKEDND	131	
QY	146	AIIPCRITDDE--TPVTLHNSGVPVASYDSRQGFNGFTVGPYI-----	168	
DB	132	TLVRCPLTDEVTNYSLKGCQG--KLPKQUR-----FIDPKAGIMIKVKRAYHRLCL	184	
QY	189	CEATVAGKGFOTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVTCAVFN-----	239	
DB	185	HCSVDQEGKSVLSEKFLKVRPAFAKVPVSVSKASY--LLREGEFTVTCTIKDVSSSV	242	
QY	240	-----NEVVDLOWTFPGVKGGITMLEEIKVPSIKLVYTLTVPEATVKDSGDVECAA	292	
DB	243	YSTWKRENSOTKQEKYNSWHHGDG-----NYERQATLTISSARVNDSGVPMCYA	292	
QY	293	RQATREVKEMKVTIISVHEKGFIEIKPTFSQLEAVNLHEVKHFWVEVRAYP--PPRISWLK	351	
DB	293	NNTFGSAN--VTTLEVDVKGFINIPMINTVFNVDNGENVDLIJEYEAFFKPEHQWIY	350	
QY	352	NNLTLENLFEITDVEKIQEIRYRSKLILIRAKBEDSGHYTIVAONEDAVKSYTPELLT	411	
DB	351	MNRFTDKWEDPKS--ENESNIRYVSELHILTRLKGTEGGTYTFLVNSDSVDNAAIAFNVV	409	
QY	412	QVPSSILD--LVDVHHGSGGTQVTCABGTPLDIEKMI CKDIKKCNNETSWTILANN	468	
DB	410	NTRPEILTYDRLVNG-----MLQCAAAGFPEPTIDWYFCGTEQ---RCASVLDPVD	458	
QY	469	VSNIITIBHSRDRSTVEGRTVFAKVEETIAVRCLAKNLLGAE-----NRELKVA	518	
DB	459	VQTLNCGSPFGFKLVQSSIDSASFANGHTVECKAVNDVGKTSAYENFAFKGNKEQIHP	518	
QY	519	PTLSELTAANAALVLLVIVIIISLIVLWVKOKPBYEIRWRVIESIPDGHEYIVVDPM	578	
DB	519	HTLFTPLLIGFVIVAGMCCIIV--MLITYKYLQKPMTEVOMKVVEEI--NGNNYVVIDPT	574	
QY	579	QLPYDSRWEPPRDLGLVGRVLGSGAFKGVVEGAYGLSRSQPMKVAVKMLKPTARSSEK	638	
DB	575	QLPYDHWEPFRNRLSPGKTLAGAGFKGVVEATAYGLIKSDAAMTAVKMLKPSAHLTER	634	
QY	639	QALMSELKIMTHLQPHNLINVLGACTKSGPIVITTEYCPYGLDYNLHKNRDSFLSHHP	698	
DB	635	EALMSELKVLISYLGNNHNNIYNLGLACTIGGPTLIVITEYCCYGDLLFLRKRRDSFCSQK	694	
QY	699	EKPKKELDIGLPADSESTSYVILSPFNNGDYMDMKQADTTOYVPMLEKREKYSYSDIQ	758	
DB	695	EDHAAALYKNLHLHSESSCS-----DSNTFNDMKPG--VSIV-----VPTKADKR	739	
QY	759	RSLYDRPASYKKXSMULDSEYKNLLSDNSEGLTLDLLSFTYQVARGMEFLASKNCVHRD	818	
DB	740	RSV--RIGS-----IERDVTPAIMDEDLALOLELLSPSYQVAKGMFLASKNCIHRD	792	
QY	819	LAARNVLLAQKIVKICDGLADIMHDSNYVSKGSTFLPKVMAPEISFDNLTYTTLSDV	878	
DB	793	LAARNILLTHGRTKICDGLARDIKNDNSYVVKGNARLPFKVMAPEISFNCVYTFESDV	852	
QY	879	WSYGILLWEIFSLGGTPYPGMWVDSTFYNKIKSGYRMKAPDHAITSVEYETMWKCNSEPE	938	
DB	853	WSYGI FLWELFSLGSSPYGPMVDYSKFYKMIKSGFRMLSPEHAPAEWYDIMKTCWADPL	912	
QY	939	KRPSFYHLSEIVENLPGQYKYSYEKI	965	
DB	913	KRPTFKQIVOLIEBKQISESTNTHYISNL	939	



F;583-591/Region: protein kinase ATP-binding motif

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Query Match      25.1%; Score 1416.5; DB 2; Length 954;
Best Local Similarity 36.4%; Pred. No. 2.6e-54;
Matches 361; Conservative 157; Mismatches 368; Indels 107; Gaps 32;

QY 26 SLPSILPNEKEKVVOLNSSFSLRCFGESEVSWOYPMSS--EESSDVIEIR--NEENNSGLF 81
DB 19 AVPKINDGERVTVVGDKVSLSRCDRLHLVILAFQSKGLMKPKRDLKSRPLNNSSETDQFF 78

QY 82 VTVLEVSSASAAHTGLTYCYNNHTQTTEENELEGRHIYIYVDPDVAFAVPLGMDTYLVIVE 141
DB 79 VII-----KADLRHLGRYIC--TWTEIQEN---TSVSLFVKDPAFPDLFPID----VT 124

QY 142 DDSALIPCTTDPETPVTILHNSG--VVPASYDSRQGFNGTFTV-----GPYICEAT 192
DB 125 EGADTVGMCPPTDMDIAIEKCDGSPLENFTFTDIEAGITIKTVQLAFDSCYVCSGN 184

QY 193 VKGKKFOTIPFNVYALKATSEL--DLEMEALKTVYKGETIVVTCAVFN--NEVVDLQWTYP 250
DB 185 KSGTVKSSFTSHVRPVKPKVTVFLSKRQLVKTGEPFEVTCALVDVFTVKAQWL-- 242

QY 251 GEVKGKGITMLBEIKVPSIKLVTLTVPEATV--KDSGDYECARQATREVEMKKVTIS 308
DB 243 -DVK-EGVTRQANFRSGNV--FSYNLTLKSDGVPYSESRTFTCOAENAIQGVN--ATFTLD 297

QY 309 VHEKGFIEIKPTSOLEAVNLHEVKHFVVEVRAYPPTIS--WLKNNLTILIENLTITDV 367
DB 298 VIDVGYVNLTVLENTTISVNAQNGLVLKVYIDAYPHDPDGVWTFYFNETLL--NTSDHYAT 356

QY 368 EKIQEIYRSKLIIRAKEDSGHYITVAQNEAVKSYTPPELLTQVPSSTLDLVDHHS 427
DB 357 KDSGNRYVSELHLIRLKGTEKGVYFTYTNSSDDASVSNIQVTKRPELLIAERTSEG-- 415

QY 428 TGGQTVRCTAEGTPLPDIEWMI CK-DIKKCNNTSMTILANNVSNITTEIHSRDRSTVEG 486
DB 416 ----TLQCATGFPVPAIOWYFCFGEQRC---TDYPLSPVNEKTIQENSSLGRIWVES 468

QY 487 RVTFKAVEETIIVRCIAKLLGAENR-----ELKLVAPTLRSELT---VAARVLLVI 537
DB 469 TIDVNDLKNKGTVOCVASNEVESAYSVFSFAIKEKLRTHTLFPLLIIGFTAAAGL----- 523

QY 538 VIISLIVLVIMVKQKPRYERIRWVIESISPDGHEIYIVDPMQLPDSRWEPFRDGLVLGR 597
DB 524 MCIAVAVLMYKYLQKPYELQWKVVEI--NGNNYVYIDTQLPYDNKWEFPEDRLCFGK 581

QY 598 VLGSAGFKVGEATAYGLSRSQPMKAVKMLKPTARSEKQALMSSELKIMTHLGHPLNI 657
DB 582 ILGAGAFKGVVEATAYGLLKEDSRLTAVAKMLKPSAHSATERALMSSELKVLVLGHHKNI 641

QY 658 VNLGACTKSGPIYIITEYCFYGLVNYLHKNRDPSLSHHPEKPK---KELDIFG--LN 711
DB 642 VNLGACTVGGPTLVITEYCCYGDLLNLRKRDSDFC-----PKPEDNSEAALYKNLLN 696

QY 712 PADESTRSYVILFENNNGDYMMDKQADTQTVVPLERKEVSKYSIDIQRSLYDRPASYYKK 771
DB 697 TRD-----MCEGMSGEIYDMKPA--VSIV-----VPTKTKERS-----G 729

QY 772 SMLDSEVKNLLSDNBSGLTLDLLSFTYQVARGMEFLASKKNCVHRDLAARNVLLAQGI 831
DB 730 SFGQDVSIVSIPREDDALDTEDLINFSYQVAGMNFASKKNCIHRDLAARNILLTHGRI 789

QY 832 VKICDFGLARDIMHDSNYSKSTFLPVKMMAPESIFDNLTYTLSDVWSYGILLWEIFSL 891
DB 790 TKICDFGLARDINDSNVYVKGNAFLPVKMMAPESIFCHVYTFESDVWSYGILLWEIFSL 849

QY 892 GGTFFPCMVMVDSTFYANKISGYRMAKPDHATSEVYEMVKMNSPEKRPSPFYHLSEIVE 951
DB 850 GSSPYPRIPVDSKFYKMIKDGWRMMSPECAPLEMWEIMRSCWNSDPLKRPFPKQIQOMVE 909

QY 952 NLLPGQYKYSYEKIHLDFLKSDHPAVARVDS 984
DB 910 Q-----QLSDSKNGNTPLPYVPVSHVPLDHAVRINS 938
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RESULT 15
TVCTMD
macrophage colony-stimulating factor 1 receptor precursor - cat
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) csflr/fms
C;Species: Felis silvestris catus (domestic cat)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: A31636
R;Woolford, J.; McAuliffe, A.; Rohrschneider, L.R.
Cell 55, 965-977, 1988
A;Title: Activation of the feline c-fms proto-oncogene: multiple alterations are required
A;Reference number: A31636; MUID:89077553; PMID:2849512
A;Accession: A31636
A;Molecule type: mRNA
A;Residues: 1-980 <WOO>
A;Cross-references: UNIPROT:PI3369; EMBL:X03663
C;Genetics:
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-980/Product: macrophage colony-stimulating factor 1 receptor #status predicted <EXT>
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F;35-96/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;410-484/Domain: immunoglobulin homology <IMM5>
F;510-534/Domain: transmembrane #status predicted <TM>
F;535-980/Domain: intracellular #status predicted <INT>
F;577-915/Domain: protein kinase homology <KIN>
F;585-593/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,417-482/Dissulfide bonds: #status predicted
F;45,73,94,153,275,302,335,410,477,490/Binding site: carboxylate (Asn) (covalent) #statu
F;613,630,776/Active site: Lys, Glu, Asp #status predicted
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match      25.0%; Score 1412.5; DB 1; Length 980;
Best Local Similarity 33.2%; Pred. No. 3.9e-54;
Matches 359; Conservative 180; Mismatches 356; Indels 185; Gaps 33;

QY 27 LPSILPNEKEKVVOLNSSFSLRCFGESEVSWOYPMSEESSDVIEIRNEENNSGLFTVILE 86
DB 20 VPVIQPSGELVVEPGETTVTLRCVNGSVENDGPTSPHWNLDLDPSS-----SILT 70

QY 87 VSSASAAHTGLTYCYNNHTQTTEENELEGRH--IYIYVDPDVAFAVPLGMDTYLVIVEDD 144
DB 71 TNNATTQNTGTVHC-----TEPGNPQGNATILYVKDPAFPKWVLAQE---VTVLEGQ 121

QY 145 SALIPCRITDP--EPTVTLHNSG--VVPASVDSRQGFNGTFTVGP-----YICEAT 192
DB 122 DALLPCLLDPALEAGVSLVRVGRPVLRQTNYSFSPWHG--FTIHKAKFTIENHVQCSAR 180

QY 193 VKGKKFOTIPFNVYALKATSEL----LEMEALKTVYKGETIVVTCAVFNNEV---VDL 245
DB 181 VDGR---TVTSMGIWLKVQKDISGPATLTLEPAELVRIQGEAAQIVCSASINDVNFVSL 237

QY 246 QWYTFGEVKGKITMLBEIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVEMKKV 305
DB 238 R---HGDTR-LTISQSDPHDNRYQKVLTLNLDHVSFDAGNYSCTATTNAWG--NHSASM 291

QY 306 TISVHEKGFIKPTSOLEAVNLHEVKHFVVEVRAYPPTISWLKN-NLTILIENLTIT 364
DB 292 VFRVESAYNLNITSQSLLQEVTVGKEVDLQVKVEAYP-----GLSEFWTVLGPFSDIQ 346

QY 365 TDVEKI---QEIRYSKLIIRAKEDSGHYITVAQNEAVKSYTPPELLTQVPSSTI--L 418
DB 347 DKLDFVTIKDYTYTSTLSLPLKSEAGRYSLAENAGQNALITFELTLRYPPEVRVTM 406

QY 419 DIVDDHHSGTGGQTVRCTAEGTPLPDIEWMI CKDIKKCNNTSMTILANNVSNITTEIHS 478
DB 419 Q-----QLSDSKNGNTPLPYVPVSHVPLDHAVRINS 938
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2005, 07:17:30 ; Search time 74.0692 Seconds  
(without alignments)  
4925.234 Million cell updates/sec

Title: US-10-027-400-4

Perfect score: 5766

Sequence: 1 MRLPGAMPALALKGELLIS.....EQLPDGCGCAPRAEDSFL 1106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*

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5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*

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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5766	100.0	1106	14	US-10-027-400-4
2	5762	99.9	1106	9	Sequence 4, Appli
3	5762	99.9	1106	15	Sequence 2, Appli
4	5762	99.9	1106	15	Sequence 51, Appli
5	5760	99.9	1106	9	Sequence 36, Appli
6	5758	99.9	1106	9	Sequence 22, Appli
7	5757	99.8	1106	9	Sequence 16, Appli
8	5756	99.8	1106	9	Sequence 20, Appli
9	5766	98.4	1090	9	Sequence 18, Appli
10	2882	50.0	561	9	Sequence 14, Appli
11	2352.5	40.8	1089	9	Sequence 10, Appli
12	2351.5	40.8	1089	9	Sequence 2, Appli
13	2351.5	40.8	1089	9	Sequence 90, Appli

14 2351.5 40.8 1089 9 US-09-866-510-2 Sequence 2, Appli

15 2351.5 40.8 1089 9 US-09-955-363-36 Sequence 36, Appli

16 2351.5 40.8 1089 14 US-10-027-400-2 Sequence 2, Appli

17 2351.5 40.8 1089 15 US-10-394-322A-50 Sequence 50, Appli

18 2351.5 40.8 1089 15 US-10-367-639-35 Sequence 35, Appli

19 2351.5 40.8 1089 16 US-10-322-698-168 Sequence 168, Appli

20 2351.5 40.8 1089 16 US-10-741-601-439 Sequence 439, Appli

21 2351.5 40.8 1089 17 US-10-741-600-1304 Sequence 1304, Appli

22 2350 40.8 1088 10 US-09-961-403-4 Sequence 4, Appli

23 2347.5 40.7 1089 9 US-09-866-510-4 Sequence 4, Appli

24 2346.5 40.7 1089 9 US-09-866-510-8 Sequence 8, Appli

25 2345.5 40.7 1089 9 US-09-866-510-6 Sequence 6, Appli

26 2342.5 39.8 1096 16 US-10-322-696-165 Sequence 165, Appli

27 1499.5 26.0 460 16 US-10-664-421-64 Sequence 64, Appli

28 1400.5 24.3 976 13 US-10-099-895-32 Sequence 32, Appli

29 1400.5 24.3 976 14 US-10-193-867-4 Sequence 4, Appli

30 1400.5 24.3 976 15 US-10-295-027-708 Sequence 708, Appli

31 1400.5 24.3 976 15 US-10-457-954-2 Sequence 2, Appli

32 1385.5 24.0 811 15 US-10-637-356-4 Sequence 4, Appli

33 1383.5 24.0 826 15 US-10-637-356-3 Sequence 3, Appli

34 1382.5 24.0 975 14 US-10-192-867-2 Sequence 2, Appli

35 1380 23.9 834 15 US-10-637-356-2 Sequence 2, Appli

36 1380 23.9 849 15 US-10-637-356-1 Sequence 1, Appli

37 1370.5 23.8 972 9 US-09-944-807-10 Sequence 10, Appli

38 1370.5 23.8 972 17 US-10-741-600-1570 Sequence 1570, Appli

39 1370.5 23.8 972 17 US-10-741-600-1571 Sequence 1571, Appli

40 1306 22.7 806 16 US-10-408-765A-2335 Sequence 2335, Appli

41 1287.5 22.3 386 9 US-09-939-754-6 Sequence 6, Appli

42 1287.5 22.3 386 9 US-09-939-832-6 Sequence 6, Appli

43 1287.5 22.3 386 9 US-09-939-833-6 Sequence 6, Appli

44 1138 19.7 1333 15 US-10-394-322A-65 Sequence 65, Appli

45 1133 19.6 1302 15 US-10-402-365-2 Sequence 2, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-027-400-4

; Sequence 4, Application US/10027400

; Publication No. US20030017535A1

; GENERAL INFORMATION:

APPLICANT: WILLIAMS, Lewis T.

ESCOBEDO, Jaime A.

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market, Steuart Street Tower, 20th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/027, 400

APPLICATION NUMBER: US/10/027, 400

FILING DATE: 19-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/461,917

FILING DATE: 05-JUN-1995

APPLICATION NUMBER: US 07/151,414

FILING DATE: 02-FEB-1988

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Karen B.

REGISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 2307K-267-2-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/326-2400

```

; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-027-400-4

Query Match      100.0%; Score 5766; DB 14; Length 1106;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRLPGAMPALALKGELLSSLLSLLLELQISQGLVWTPPGPELVNVSSTVFLTCSGAPV 60

QY 61 VWRMSQEPQEMAKAQDGFSSVLTNLTLTGLDTGTFCTHNSRGLTDERKRLYIFV 120
DB 61 VWRMSQEPQEMAKAQDGFSSVLTNLTLTGLDTGTFCTHNSRGLTDERKRLYIFV 120

QY 121 PDPTVGLPNDABELFIFLFEITTEITIPCRVTPDQLVVTLHEKKGVDVALPVPYDHQGF 180
DB 121 PDPTVGLPNDABELFIFLFEITTEITIPCRVTPDQLVVTLHEKKGVDVALPVPYDHQGF 180

QY 181 GIFEDRSYICKTIGREVDSDAYVYRLOVSSINVSNAVQTVRQGENITLMCVIGN 240
DB 181 GIFEDRSYICKTIGREVDSDAYVYRLOVSSINVSNAVQTVRQGENITLMCVIGN 240

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DB 241 DVNFEWTPRKSGRLVEPVTDFLLDMPYHISILHPSAELEDSGTTCNTVESVNDH 300

QY 301 QDEKAINITVSGYVLLGEVGTLOFAELHRRTLOVFEAYPPPTVLMFKDNRITLGD 360
DB 301 QDEKAINITVSGYVLLGEVGTLOFAELHRRTLOVFEAYPPPTVLMFKDNRITLGD 360

QY 361 SAGEIALSTNVSETRYVSLTLVRVKVAAGHYTWRAFHEDAEVQLSFOLQINVPVRVL 420
DB 361 SAGEIALSTNVSETRYVSLTLVRVKVAAGHYTWRAFHEDAEVQLSFOLQINVPVRVL 420

QY 421 ELSHSDPDSGEQVRCRGRGMPQNIWASCRDLKRCRELPTLLGNSSEESQLETVN 480
DB 421 ELSHSDPDSGEQVRCRGRGMPQNIWASCRDLKRCRELPTLLGNSSEESQLETVN 480

QY 481 TYWEEBOEFVSTLRLOHVDRLPVSRCCTLRNAVQDQTQEVIVVPHSLPKVWVISA 540
DB 481 TYWEEBOEFVSTLRLOHVDRLPVSRCCTLRNAVQDQTQEVIVVPHSLPKVWVISA 540

QY 541 LVVLTISLILMLWKKPRYELRWKVIKESVSDGHEIYVDPMQLPYDSTWELPRDQL 600
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DB 721 PVGLPLPSHVSLSGESGGYMDSKDESVDVPMKMDKGVKYADIESSNYPYNYVP 780

QY 781 SAPERTCRATILINESPVLSDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICGKLV 840
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QY 841 KICDFGLARDIMRDSNYISKGSTPLPLKWMAPSIFFNSLYTTLSDVWVSFGILLWEIPTLG 900
DB 841 KICDFGLARDIMRDSNYISKGSTPLPLKWMAPSIFFNSLYTTLSDVWVSFGILLWEIPTLG 900

; US-09-955-363-2
; Sequence 2, Application US/09955363
; Patent No. US2002017362A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; Kindvogel Ph.D., Wayne R.
; Bell, Lillian A.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/955,363
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-955-363-2

Query Match      99.9%; Score 5762; DB 9; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRLPGAMPALAKGELLALLSLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCSSAPV 60  
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QY 121 PDPTVGLPNDABELFIFLITEITIPCRVTDQPLVLTLLHEKKGVALPVPYDHOGRFS 180  
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QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTMRAPFHEDAEVQLSFOLQINVPVRL 420  
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTMRAPFHEDAEVQLSFOLQINVPVRL 420  
QY 421 ELSSEHPDSEGTVCRCRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480  
Db 421 ELSSEHPDSEGTVCRCRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480  
QY 481 TYWEEQEPEFVSTLRLOHVDRLPLSRCTLRNAGQDTQEVIVVPHSLPKVQVVISAILA 540  
Db 481 TYWEEQEPEFVSTLRLOHVDRLPLSRCTLRNAGQDTQEVIVVPHSLPKVQVVISAILA 540  
QY 541 LVVLTIIISLIIILMLQKKPRYIRWKVIESVSDGHEIYVYDPMQLPYDSTWELPRDQL 600  
Db 541 LVVLTIIISLIIILMLQKKPRYIRWKVIESVSDGHEIYVYDPMQLPYDSTWELPRDQL 600  
QY 601 VLGRITLGSAGFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660  
Db 601 VLGRITLGSAGFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660  
QY 661 HLNVNLLGACTKGGPYIITEICRYGDLVDYLHRNKHTFLQHSKRRPPSAELYSNAL 720  
Db 661 HLNVNLLGACTKGGPYIITEICRYGDLVDYLHRNKHTFLQHSKRRPPSAELYSNAL 720

Db 1081 EPEPELEQLPDSCGPAPRAEDSFL 1106  
RESULT 3  
US-10-394-322A-51  
; Sequence 51, Application US/10394322A  
; Publication No. US20030232391A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.  
; APPLICANT: Prescott, John C.  
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS  
; FILE REFERENCE: 39750-0006 US  
; CURRENT APPLICATION NUMBER: US/10/394,322A  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,892  
; FILING DATE: 2002-03-21  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 1106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-322A-51  
Query Match 99.9%; Score 5762; DB 15; Length 1106;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRLPGAMPALAKGELLALLSLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCSSAPV 60  
Db 1 MRLPGAMPALAKGELLALLSLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCSSAPV 60  
QY 61 VWERMSQEPPOEMAKAQDGTFFSSVLTLTNLTLGLDTGEYFCTHNDNRGLTDERKRLYIFV 120  
Db 61 VWERMSQEPPOEMAKAQDGTFFSSVLTLTNLTLGLDTGEYFCTHNDNRGLTDERKRLYIFV 120  
QY 121 PDPTVGLPNDABELFIFLITEITIPCRVTDQPLVLTLLHEKKGVALPVPYDHOGRFS 180  
Db 121 PDPTVGLPNDABELFIFLITEITIPCRVTDQPLVLTLLHEKKGVALPVPYDHOGRFS 180  
QY 181 GIFEDRSYCKTTIGREVSDSDAYVYRLOVSSINVSNAVQTVRQGENITLWCIVGN 240  
Db 181 GIFEDRSYCKTTIGREVSDSDAYVYRLOVSSINVSNAVQTVRQGENITLWCIVGN 240  
QY 241 DVNFWEFTYPRKESGRVLEPVTDFLLDMPYHRSILHIPSAAELEDSTYTCNVTESVNDH 300  
Db 241 DVNFWEFTYPRKESGRVLEPVTDFLLDMPYHRSILHIPSAAELEDSTYTCNVTESVNDH 300  
QY 301 QDEKAINITVWESGYVRLLEGEVGTLOFAELHRSRTLQVFEAYPPPTVLMFKDNRITLGD 360  
Db 301 QDEKAINITVWESGYVRLLEGEVGTLOFAELHRSRTLQVFEAYPPPTVLMFKDNRITLGD 360  
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTMRAPFHEDAEVQLSFOLQINVPVRL 420  
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTMRAPFHEDAEVQLSFOLQINVPVRL 420  
QY 421 ELSSEHPDSEGTVCRCRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480  
Db 421 ELSSEHPDSEGTVCRCRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480  
QY 481 TYWEEQEPEFVSTLRLOHVDRLPLSRCTLRNAGQDTQEVIVVPHSLPKVQVVISAILA 540  
Db 481 TYWEEQEPEFVSTLRLOHVDRLPLSRCTLRNAGQDTQEVIVVPHSLPKVQVVISAILA 540  
QY 541 LVVLTIIISLIIILMLQKKPRYIRWKVIESVSDGHEIYVYDPMQLPYDSTWELPRDQL 600  
Db 541 LVVLTIIISLIIILMLQKKPRYIRWKVIESVSDGHEIYVYDPMQLPYDSTWELPRDQL 600  
QY 601 VLGRITLGSAGFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660  
Db 601 VLGRITLGSAGFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660  
QY 661 HLNVNLLGACTKGGPYIITEICRYGDLVDYLHRNKHTFLQHSKRRPPSAELYSNAL 720  
Db 661 HLNVNLLGACTKGGPYIITEICRYGDLVDYLHRNKHTFLQHSKRRPPSAELYSNAL 720

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Db      661  HLNVNLLGACTGGPIYIIITEYCRYGDLVDYLHNRKHTFLQHSDDKRRPPSAELYSNAL 720
Qy      721  PVGLPLPSHVSITGESGGYMDSKDSVDYVPMMDKMGDKVYADIESSNYMAPYDNYVP 780
Db      721  PVGLPLPSHVSITGESGGYMDSKDSVDYVPMMDKMGDKVYADIESSNYMAPYDNYVP 780
Qy      781  SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLIICEGLV 840
Db      781  SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLIICEGLV 840
Qy      841  KICDFGLARDIMRDSNYISKGSFTPLPKWMAPEISFNSLYTTLSDVMSFGILLWEIPTLG 900
Db      841  KICDFGLARDIMRDSNYISKGSFTPLPKWMAPEISFNSLYTTLSDVMSFGILLWEIPTLG 900
Qy      901  GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYIMQKWEKFEIRPPFSQVLVLLER 960
Db      901  GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYIMQKWEKFEIRPPFSQVLVLLER 960
Qy      961  LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVOPNEGND 1020
Db      961  LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVOPNEGND 1020
Qy      1021  YIIPDPKPPEVADEGLESPSLASSTLNEVNTSSTICDSPLEPQDEPEPEPQLEQV 1080
Db      1021  YIIPDPKPPEVADEGLESPSLASSTLNEVNTSSTICDSPLEPQDEPEPEPQLEQV 1080
Qy      1081  EPEPELQPDGCPAPRAEADSFL 1106
Db      1081  EPEPELQPDGCPAPRAEADSFL 1106

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RESULT 4

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US-10-367-639-36
; Sequence 36, Application US/10367639
; Publication No. US20040001807A1
; GENERAL INFORMATION:
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Edelberg, Jay M.
; APPLICANT: Rafii, Shahin
; APPLICANT: Hong, Mun K.
; APPLICANT: Lanza, Robert P.
; APPLICANT: West, Michael D.
; TITLE OF INVENTION: Endothelial Precursor Cells for Enhancing and Restoring Vascular
; FILE REFERENCE: 1676.004US1
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 1106
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-367-639-36

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Query Match      99.9%; Score 5762; DB 15; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MRLPGAMPALAKGELLILLLEPQISQGLVWTPPGPELVNVSSTFVLTCSGAPV 60
Db      1  MRLPGAMPALAKGELLILLLEPQISQGLVWTPPGPELVNVSSTFVLTCSGAPV 60

Qy      61  VWRMSQEPQEWAKAQDGTFSSVLTNTLTGDTGEYFCTHNDNRGLTDERKRLYIFV 120
Db      61  VWRMSQEPQEWAKAQDGTFSSVLTNTLTGDTGEYFCTHNDNRGLTDERKRLYIFV 120

Qy      121  PDPTVGLPNDABELFIFLFEITITICRVTDPQLVWTLHEKKGDVALPVPYDHORGFS 180
Db      121  PDPTVGLPNDABELFIFLFEITITICRVTDPQLVWTLHEKKGDVALPVPYDHORGFS 180

Qy      181  GIFEDRSYICKTTIGREVSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIIVGN 240

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RESULT 5

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US-09-866-510-22
; Sequence 22, Application US/09866510
; Patent No. US2002011304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510

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Db      181  GIFEDRSYICKTTIGREVSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIIVGN 240
Qy      241  DVNVFEMWTPRKESGRLVPEVPTDFFLLDMPVHRSIIHIHPSAELEDSGTTCNVTESVNDH 300
Db      241  EVNVFEMWTPRKESGRLVPEVPTDFFLLDMPVHRSIIHIHPSAELEDSGTTCNVTESVNDH 300
Qy      301  QDEKAINITIVBESGYVRLLEGEVGTLOFAELHRSRTLQVVFAYPPPTVLMFKDNRITLGD 360
Db      301  QDEKAINITIVBESGYVRLLEGEVGTLOFAELHRSRTLQVVFAYPPPTVLMFKDNRITLGD 360
Qy      361  SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTNRAFHEDAEOVLSQQLQINVPVRL 420
Db      361  SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTNRAFHEDAEOVLSQQLQINVPVRL 420
Qy      421  ELSHSDPDGSEOTVRCRGRMPQPNIIWSACRDLKCPRELPTLLGNSEESQLETVN 480
Db      421  ELSHSDPDGSEOTVRCRGRMPQPNIIWSACRDLKCPRELPTLLGNSEESQLETVN 480
Qy      481  TYWEESEQEFVWSTLRLQHVDRPLSVRCCTLRNAVGDQTOEVIIVPHSLPFKVVVISAILA 540
Db      481  TYWEESEQEFVWSTLRLQHVDRPLSVRCCTLRNAVGDQTOEVIIVPHSLPFKVVVISAILA 540
Qy      541  LVVLTIIISIIILIMLWQKPRYEIRWKVIESVSSDGHYIYVDPMDQLPYDSTWELPRDQL 600
Db      541  LVVLTIIISIIILIMLWQKPRYEIRWKVIESVSSDGHYIYVDPMDQLPYDSTWELPRDQL 600
Qy      601  VLGRITLGSAGFQGVVEATAGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Db      601  VLGRITLGSAGFQGVVEATAGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
Qy      661  HLNVNLLGACTGGPIYIIITEYCRYGDLVDYLHNRKHTFLQHSDDKRRPPSAELYSNAL 720
Db      661  HLNVNLLGACTGGPIYIIITEYCRYGDLVDYLHNRKHTFLQHSDDKRRPPSAELYSNAL 720
Qy      721  PVGLPLPSHVSITGESGGYMDSKDSVDYVPMMDKMGDKVYADIESSNYMAPYDNYVP 780
Db      721  PVGLPLPSHVSITGESGGYMDSKDSVDYVPMMDKMGDKVYADIESSNYMAPYDNYVP 780
Qy      781  SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLIICEGLV 840
Db      781  SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLIICEGLV 840
Qy      841  KICDFGLARDIMRDSNYISKGSFTPLPKWMAPEISFNSLYTTLSDVMSFGILLWEIPTLG 900
Db      841  KICDFGLARDIMRDSNYISKGSFTPLPKWMAPEISFNSLYTTLSDVMSFGILLWEIPTLG 900
Qy      901  GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYIMQKWEKFEIRPPFSQVLVLLER 960
Db      901  GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYIMQKWEKFEIRPPFSQVLVLLER 960
Qy      961  LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVOPNEGND 1020
Db      961  LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVOPNEGND 1020
Qy      1021  YIIPDPKPPEVADEGLESPSLASSTLNEVNTSSTICDSPLEPQDEPEPEPQLEQV 1080
Db      1021  YIIPDPKPPEVADEGLESPSLASSTLNEVNTSSTICDSPLEPQDEPEPEPQLEQV 1080
Qy      1081  EPEPELQPDGCPAPRAEADSFL 1106
Db      1081  EPEPELQPDGCPAPRAEADSFL 1106

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; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-22

Query Match          99.9%; Score 5760; DB 9; Length 1106;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1104; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPGAMPALAKGELLSSLLSLLLEBPQISQGLVWTPPGPELVNVSSTFVLTCSGAPV 60
DB 1 MRLPGAMPALAKGELLSSLLSLLLEBPQISQGLVWTPPGPELVNVSSTFVLTCSGAPV 60

QY 61 VWERMSQEPPOEMAKAQDGFSSVLTNLTLTGLDTGEYFCTHNDSSRGLETDERKRLYIFV 120
DB 61 VWERMSQEPPOEMAKAQDGFSSVLTNLTLTGLDTGEYFCTHNDSSRGLETDERKRLYIFV 120

QY 121 PDPTVGFPLNDABELFIFLITEITIPCRVTPDQLVWTLHEKKGDDVALPVPYDHOGRGFS 180
DB 121 PDPTVGFPLNDABELFIFLITEITIPCRVTPDQLVWTLHEKKGDDVALPVPYDHOGRGFS 180

QY 181 GIFEDRSYCKTTIGREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240
DB 181 GIFEDRSYCKTTIGREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240

QY 241 DVNFWFTYPRKESGRVVEPTDPLDMPYHISILHI PSAELEDSTYTCNVTESVNDH 300
DB 241 DVNFWFTYPRKESGRVVEPTDPLDMPYHISILHI PSAELEDSTYTCNVTESVNDH 300

QY 301 QDEKAINITVWESGYVRLGEGVTLQFAELHRSRTLQVWFEAYPPPTVLMFKDNRITLGD 360
DB 301 QDEKAINITVWESGYVRLGEGVTLQFAELHRSRTLQVWFEAYPPPTVLMFKDNRITLGD 360

QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTWRAFHEDAEVQLSFOLQINVPVRVL 420
DB 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTWRAFHEDAEVQLSFOLQINVPVRVL 420

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-16

Query Match          99.9%; Score 5758; DB 9; Length 1106;
Best Local Similarity 99.8%; Pred. No. 6.2e-318;
Matches 1104; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPGAMPALAKGELLSSLLSLLLEBPQISQGLVWTPPGPELVNVSSTFVLTCSGAPV 60
DB 1 MRLPGAMPALAKGELLSSLLSLLLEBPQISQGLVWTPPGPELVNVSSTFVLTCSGAPV 60

QY 61 VWERMSQEPPOEMAKAQDGFSSVLTNLTLTGLDTGEYFCTHNDSSRGLETDERKRLYIFV 120
DB 61 VWERMSQEPPOEMAKAQDGFSSVLTNLTLTGLDTGEYFCTHNDSSRGLETDERKRLYIFV 120

QY 121 PDPTVGFPLNDABELFIFLITEITIPCRVTPDQLVWTLHEKKGDDVALPVPYDHOGRGFS 180
DB 121 PDPTVGFPLNDABELFIFLITEITIPCRVTPDQLVWTLHEKKGDDVALPVPYDHOGRGFS 180

QY 181 GIFEDRSYCKTTIGREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240
DB 181 GIFEDRSYCKTTIGREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240

QY 241 DVNFWFTYPRKESGRVVEPTDPLDMPYHISILHI PSAELEDSTYTCNVTESVNDH 300
DB 241 DVNFWFTYPRKESGRVVEPTDPLDMPYHISILHI PSAELEDSTYTCNVTESVNDH 300

QY 301 QDEKAINITVWESGYVRLGEGVTLQFAELHRSRTLQVWFEAYPPPTVLMFKDNRITLGD 360
DB 301 QDEKAINITVWESGYVRLGEGVTLQFAELHRSRTLQVWFEAYPPPTVLMFKDNRITLGD 360

QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTWRAFHEDAEVQLSFOLQINVPVRVL 420
DB 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTWRAFHEDAEVQLSFOLQINVPVRVL 420

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Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQQLQINVPVRVL 420
Qy 421 ELSSEHPDSEGEQVRCRGKMPQPNIIWSACRDLKRCPRLEPPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSEGEQVRCRGKMPQPNIIWSACRDLKRCPRLEPPTLLGNSSEESQLETNV 480
Qy 481 TYWEEQEEFEVSTLRLQHVDRPLSVRCRTLRNAVGQDTQEVIVVPHSLPKVVI SAILA 540
Db 481 TYWEEQEEFEVSTLRLQHVDRPLSVRCRTLRNAVGQDTQEVIVVPHSLPKVVI SAILA 540
Qy 541 LVVLTITISLIILMLQKKPRYIEIRWKVIESVSSDGEHYIYVDPMLPYDSTWELPRDQL 600
Db 541 LVVLTITISLIILMLQKKPRYIEIRWKVIESVSSDGEHYIYVDPMLPYDSTWELPRDQL 600
Qy 601 VLGRITLGSAGFGQVVEATAGHLSQATMKVAVKMLKSTARSEKQALMSKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVVEATAGHLSQATMKVAVKMLKSTARSEKQALMSKIMSHLGP 660
Qy 661 HLNVNLLGACTKGGPIIITEYCRYGDLDVYLHRNKHTFLOHHSKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIIITEYCRYGDLDVYLHRNKHTFLOHHSKRRPPSAELYSNAL 720
Qy 721 PVGLPLPSSHVSLTGESDGGYMDMSKDESVDYVPMKMGDKVYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSSHVSLTGESDGGYMDMSKDESVDYVPMKMGDKVYADIESSNYMAPYDNYVP 780
Qy 781 SAPERTCRATLINESPVLSDVGFYSQVANGMEFLASKNCVHRDLAARNVLCGKLV 840
Db 781 SAPERTCRATLINESPVLSDVGFYSQVANGMEFLASKNCVHRDLAARNVLCGKLV 840
Qy 841 KICDFGLARDIMRDSNVISKGSTFLPLKWMAPESIFNSLYTLLSDVMSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNVISKGSTFLPLKWMAPESIFNSLYTLLSDVMSFGILLWEIFTLG 900
Qy 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLLER 960
Qy 961 LLEGYKKYQVQVDEEFLRSDHPAILRSQARLPFGHGLRSPDLTSSVLYTAVQNEGDND 1020
Db 961 LLEGYKKYQVQVDEEFLRSDHPAILRSQARLPFGHGLRSPDLTSSVLYTAVQNEGDND 1020

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RESULT 7

```

US-09-866-510-20
; Sequence 20, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1106
; TYPE: PR1
; ORGANISM: Homo sapiens

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US-09-866-510-20
Query Match 99.8%; Score 5757; DB 9; Length 1106;
Best Local Similarity 99.8%; Pred. No. 6.2e-318; Mismatches 0; Indels 0; Gaps 0;
Matches 1104; Conservative 2;
Qy 1 MRLPGAMPALAKGELLMLLSLLLLLEPQISQGLVVTTPGPELVINVSSTFVLTCGSA 60
Db 1 MRLPGAMPALAKGELLMLLSLLLLLEPQISQGLVVTTPGPELVINVSSTFVLTCGSA 60
Qy 61 VVERMSQEPPOEMAQADGTFSSVLTLTNLTGLDTGEYFCTHNDSGLETDEKRLIYIFV 120
Db 61 VVERMSQEPPOEMAQADGTFSSVLTLTNLTGLDTGEYFCTHNDSGLETDEKRLIYIFV 120
Qy 121 PPTVGFPLNDABEELFIFLTELTEITIPCRVTDQVLVTLHEKKGVALPVPYDHORGFS 180
Db 121 PPTVGFPLNDABEELFIFLTELTEITIPCRVTDQVLVTLHEKKGVALPVPYDHORGFS 180
Qy 181 GIFEDRSYICKTTIGDREVDSDAYYYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYYYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240
Qy 241 DVNFWTTPRKESGRLEVPVTDFFLDMPYHIRSLIHIHPSAELEDSGTTCNTVSVNDH 300
Db 241 DVNFWTTPRKESGRLEVPVTDFFLDMPYHIRSLIHIHPSAELEDSGTTCNTVSVNDH 300
Qy 301 QDEKAINITVSEGYVRLIGEVTLOFAELHRSRTLOVFEAYPPPTVLMFKDNRITLGD 360
Db 301 QDEKAINITVSEGYVRLIGEVTLOFAELHRSRTLOVFEAYPPPTVLMFKDNRITLGD 360
Qy 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQQLQINVPVRVL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQQLQINVPVRVL 420
Qy 421 ELSSEHPDSEGEQVRCRGKMPQPNIIWSACRDLKRCPRLEPPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSEGEQVRCRGKMPQPNIIWSACRDLKRCPRLEPPTLLGNSSEESQLETNV 480
Qy 481 TYWEEQEEFEVSTLRLQHVDRPLSVRCRTLRNAVGQDTQEVIVVPHSLPKVVI SAILA 540
Db 481 TYWEEQEEFEVSTLRLQHVDRPLSVRCRTLRNAVGQDTQEVIVVPHSLPKVVI SAILA 540
Qy 541 LVVLTITISLIILMLQKKPRYIEIRWKVIESVSSDGEHYIYVDPMLPYDSTWELPRDQL 600
Db 541 LVVLTITISLIILMLQKKPRYIEIRWKVIESVSSDGEHYIYVDPMLPYDSTWELPRDQL 600
Qy 601 VLGRITLGSAGFGQVVEATAGHLSQATMKVAVKMLKSTARSEKQALMSKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVVEATAGHLSQATMKVAVKMLKSTARSEKQALMSKIMSHLGP 660
Qy 661 HLNVNLLGACTKGGPIIITEYCRYGDLDVYLHRNKHTFLOHHSKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTKGGPIIITEYCRYGDLDVYLHRNKHTFLOHHSKRRPPSAELYSNAL 720
Qy 721 PVGLPLPSSHVSLTGESDGGYMDMSKDESVDYVPMKMGDKVYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSSHVSLTGESDGGYMDMSKDESVDYVPMKMGDKVYADIESSNYMAPYDNYVP 780
Qy 781 SAPERTCRATLINESPVLSDVGFYSQVANGMEFLASKNCVHRDLAARNVLCGKLV 840
Db 781 SAPERTCRATLINESPVLSDVGFYSQVANGMEFLASKNCVHRDLAARNVLCGKLV 840
Qy 841 KICDFGLARDIMRDSNVISKGSTFLPLKWMAPESIFNSLYTLLSDVMSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNVISKGSTFLPLKWMAPESIFNSLYTLLSDVMSFGILLWEIFTLG 900
Qy 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLLER 960
Qy 961 LLEGYKKYQVQVDEEFLRSDHPAILRSQARLPFGHGLRSPDLTSSVLYTAVQNEGDND 1020
Db 961 LLEGYKKYQVQVDEEFLRSDHPAILRSQARLPFGHGLRSPDLTSSVLYTAVQNEGDND 1020

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Db 61 VWRMSQEPQEMAKAQDGTSSVLTNLTLGLDTGEYFCTHNSRGLTDERKRLYIFV 120
Qy 121 PDPTVGLPNDABELFLFTEITEITIPCRVTDPOLVWTLHEKKGVALPVVDHQRGFS 180
Db 121 PDPTVGLPNDABELFLFTEITEITIPCRVTDPOLVWTLHEKKGVALPVVDHQRGFS 180
Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVRGENITLMCVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVRGENITLMCVIGN 240
Qy 241 DVNFWTYPRKESGRVPEVTDPLDMPYHRSILHIPSARELSDSGTYTCNVTSVNDH 300
Db 241 EVNFWTYPRKESGRVPEVTDPLDMPYHRSILHIPSARELSDSGTYTCNVTSVNDH 300
Qy 301 ODEKAINITVBSGYVRLLEGEVGTQFAELHRSRTLOVFEAYPPPTVLFKDNRTLGD 360
Db 301 ODEKAINITVBSGYVRLLEGEVGTQFAELHRSRTLOVFEAYPPPTVLFKDNRTLGD 360
Qy 361 SAGEIALSTRNVSETRYVSELTLVRKVAEAGHYTMRAFHEDEAVQLSFQQLINVPVRL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRKVAEAGHYTMRAFHEDEAVQLSFQQLINVPVRL 420
Qy 421 ELSHSDSGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480
Db 421 ELSHSDSGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480
Qy 481 TYWEEEOEFVSTLRLOHVDRLPVSCTLRNAVQDQTEVIVVPHSLPKVVIISAILA 540
Db 481 TYWEEEOEFVSTLRLOHVDRLPVSCTLRNAVQDQTEVIVVPHSLPKVVIISAILA 540
Qy 541 LVVLTIIISLIILMLWQKKPR 561
Db 541 LVVLTIIISLIILMLWQKKPR 561
Qy 601 VLGRITLGSAGFQVVEATAGHLSQATMKVAVMLKSTARSSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFQVVEATAGHLSQATMKVAVMLKSTARSSEKQALMSELKIMSHLGP 660
Qy 661 HLNVNLLGACTGGPIYIITECRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
Db 661 HLNVNLLGACTGGPIYIITECRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
Qy 721 PVGLPLPSHVSLSGSDGYMDMSKDESVDYVPMMDKMGDKVYADIESSNMAYPDNYVP 780
Db 721 PVGLPLPSHVSLSGSDGYMDMSKDESVDYVPMMDKMGDKVYADIESSNMAYPDNYVP 780
Qy 781 SAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLI CEGKLV 840
Db 781 SAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLI CEGKLV 840
Qy 841 KICDFGLARDIMRDSNYSIKGSTFLPLKWPAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYSIKGSTFLPLKWPAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900
Qy 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEMQKWEKFEIRPPFSQVLLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEMQKWEKFEIRPPFSQVLLLER 960
Qy 961 LLEGYKKYQVDEEFLRSDHFAILRSQARLGFHGLRSPDTSVLYTAVOPNEGDND 1020
Db 961 LLEGYKKYQVDEEFLRSDHFAILRSQARLGFHGLRSPDTSVLYTAVOPNEGDND 1020
Qy 1021 YIIPDPKPEVADEGLEPSPLASTLNENVTSTISCDSPLEQDEPEPEPQLEQV 1080
Db 1021 YIIPDPKPEVADEGLEPSPLASTLNENVTSTISCDSPLEQDEPEPEPQLEQV 1080
Qy 1081 EPEPELEQLP 1090
Db 1081 EPEPELEQLP 1090

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RESULT 10

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US-09-866-510-24
; Sequence 24, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-24

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Query Match 50.0%; Score 2882; DB 9; Length 561;
Best Local Similarity 99.8%; Pred. No. 2.2e-155;
Matches 560; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRLPGAMPALALKGELLALLSLLLELPQISQGLVVTTPGPELVNLVNSSTFVLTCSSAPV 60
Db 1 MRLPGAMPALALKGELLALLSLLLELPQISQGLVVTTPGPELVNLVNSSTFVLTCSSAPV 60
Qy 61 VWRMSQEPQEMAKAQDGTSSVLTNLTLGLDTGEYFCTHNSRGLTDERKRLYIFV 120
Db 61 VWRMSQEPQEMAKAQDGTSSVLTNLTLGLDTGEYFCTHNSRGLTDERKRLYIFV 120
Qy 121 PDPTVGLPNDABELFLFTEITEITIPCRVTDPOLVWTLHEKKGVALPVVDHQRGFS 180
Db 121 PDPTVGLPNDABELFLFTEITEITIPCRVTDPOLVWTLHEKKGVALPVVDHQRGFS 180
Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVRQENITLMCVIGN 240
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVRQENITLMCVIGN 240
Qy 241 DVNFWTYPRKESGRVPEVTDPLDMPYHRSILHIPSARELSDSGTYTCNVTSVNDH 300
Db 241 EVNFWTYPRKESGRVPEVTDPLDMPYHRSILHIPSARELSDSGTYTCNVTSVNDH 300
Qy 301 ODEKAINITVBSGYVRLLEGEVGTQFAELHRSRTLOVFEAYPPPTVLFKDNRTLGD 360
Db 301 ODEKAINITVBSGYVRLLEGEVGTQFAELHRSRTLOVFEAYPPPTVLFKDNRTLGD 360
Qy 361 SAGEIALSTRNVSETRYVSELTLVRKVAEAGHYTMRAFHEDEAVQLSFQQLINVPVRL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRKVAEAGHYTMRAFHEDEAVQLSFQQLINVPVRL 420
Qy 421 ELSHSDSGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480
Db 421 ELSHSDSGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480
Qy 481 TYWEEEOEFVSTLRLOHVDRLPVSCTLRNAVQDQTEVIVVPHSLPKVVIISAILA 540
Db 481 TYWEEEOEFVSTLRLOHVDRLPVSCTLRNAVQDQTEVIVVPHSLPKVVIISAILA 540
Qy 541 LVVLTIIISLIILMLWQKKPR 561
Db 541 LVVLTIIISLIILMLWQKKPR 561

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RESULT 11
US-09-866-510-10
; Sequence 10, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS

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APPLICANT: IKUNO, YASUSHI  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES  
FILE REFERENCE: ERM-104.01  
CURRENT APPLICATION NUMBER: US/09/866,510  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/250,747  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 60/289,103  
PRIOR FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 10  
LENGTH: 1089  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-866-510-10

Query Match 40.8%; Score 2352.5; DB 9; Length 1089;  
Best Local Similarity 44.0%; Pred. No. 5.6e-125;  
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;

Qy 8 PALALKEGELL-LSLALLEPQISQGLVTPPGPELVNVSSTFVLTCGSAFVWVE-RM 65  
Db 6 PAFVLGCLLTGSLILC---QLSLPSIL-PNENEKVQLNSFSRLRCFGESEVSWQYPM 61

Qy 66 SQPPQEM-----AKAQDGTSSVLTNLTLGDTGEYFCTHNSRGLTDT-ERKRLYIFV 120  
Db 62 SEESDSVIRNEENNSGLFVTVLEVSSASAHTGLTYCYNNHTQTEENELEGRHIYIV 121

Qy 121 PDPTVGLPNDABELFIFLITEITPCRTVDPQLVTLHEKKGDVALPVVDHORGFS 180  
Db 122 PPDVAFVPLGMDTYLVIVEDDSSAIIIPCKRTPTETVTLNHSGL---VWPASYDSRQGFN 179

Qy 181 GIFEDRSYIKTTIGREVSDSYVYVRLQVSS-INVSNVAVOTVVRQGENITLMCVIG 239  
Db 180 GTTVGPICEATVKGKFTIPFNVALKATSELDLEALKTVYKSGEITVTCVFN 239

Qy 240 NDVNVFETVPRKESGR---LVEPVTDFLLDMPYHIRSLIHPSABLEDSGTYTCNVTES 296  
Db 240 NEVVLDQWTVGVBKGKGTMLBEIKVPSIKLVY---TLTVPATVKGSDGYECAARQA 295

Qy 297 VNDHQDEKAINIVVSGYVRLGEGVTLOFABLHRSRTLOVFEAYPPPTVWFQDNRT 356  
Db 296 TREVKEMKVTISVHEKGFIEIKPTFSQEAENVLHEVKHFVVRAYPPPRISMLKNLTL 355

Qy 357 LGDSSAGETALSRTNSETRYVSELTVRVKVAEAGHYTWRAFHEDAQVLSFQLOINVP 416  
Db 356 LIENLT-EITTDVEKIQEIRYRSLKLIRAKEEDSGHYTIVAQNEAVKSYTFELLTQVP 414

Qy 417 VRVLESESHPDG-GEQTVRCRGRGMFPQPNIIWSACRDLKRCRPRELPPTLLGNS----- 469  
Db 415 SSILDVDDHHGSGTGQTVRCAETGTPLPDIEWMICKDKCNKNETSWTILANNVSNIT 474

Qy 470 ---SEESQLENTVTVWEEQEFVSVTLRLQVDRPLSVRCVTLRNAVGQDTQEVIVVPH 526  
Db 475 EITHRSRSTVEGRVTP-----AKVEETIAVRCLAKLLGAENRELKLAVP 519

Qy 527 SLFPKVVVSAIALAVLVTIISLILMLWQKPRYEIRWKVIESVSSDGHYIYVDPMQ 586  
Db 520 TLESELVAAVLLVIVIVISILVIVWQKPRYEIRWRVIESIPDGHYIYVDPMQ 579

Qy 587 LPYDSTWELPRDQVLGRTLGSAFGQVVEATAGLSHQATMKVAVKMLKSTARSSEKQ 646  
Db 580 LPYDSRWEPRDGLVLRVLGSAFGVVEGTAYGLSRSPVMKVAVKMLKPTARSSEKQ 639

Qy 647 ALMSELKIMSHLGPLHNVNLLGACTYKGGPIIITHCYCRGDLVDVYLHKNKHTFLOHSD 706  
Db 640 ALMSELKIMTHLGPLHNLVNLGACTYKGGPIIITHCYCRGDLVDVYLHKNRDSFLSHPE 699

Qy 707 KRRPPSAEYLSNAL-PVGLPLPSHVSITGSDGGMDSKDESDVYVPMMLDMKGDVKYAD 765  
Db 700 K---PKKELDIFGLNPADESTRYVILSFENNGDYMDMKQADTTQVPMLEKVEVSKYSD 756

Qy 766 IESNTYMAPYDNYVPAPERTCRATLINE-SPVLSYMDLVGFSPYQVANGMEFLASKNCVH 824  
Db 757 IQRSLYDRPASYYKKKMLSDSEVNLLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVH 816

Qy 825 RDLAARNVLICECKLVKICDFGLARDIMRDSNYSIKGSTFLPLKWMAPESIFNSLYTTL 884  
Db 817 RDLAARNVLLAQCKIVKICDFGLARDIMHDSNVKSGSTFLPKMKWAPESIFDNLXTTL 876

Qy 885 DVMSFGILLWEIETLGTTPPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMOKCWEEK 944  
Db 877 DWMSYGLLWEIETLGTTPPGMVDSTFNKIKSGYRMAKPDHATSEVVEIMVKCNSE 936

Qy 945 FEIRPPFSQVLVLLERLLGEGYKQYQVDEBFLRSDHPAILRSQARLPFGHLRSPLDT 1004  
Db 937 PEKRPSFYHLSEIVENLLPQYKYSYEKIHLDLKDHPAVARMR-----VDS 984

Qy 1005 SSVLYTAVQPN-----GDNDYIIPLP---DPKPEVADSGPLGSPSLA 1045  
Db 985 DNAYIGVTVYKNEEDKLKOWEGGLDEORLSADSGYIIPLPDIDVPVEEDLGKKNRHSSQT 1044

Qy 1046 S---STLNEVNTSTISCDSPLEPQDEPEPEPQLEOVEPEPELEQLPDSCGAPRAEAE 1103  
Db 1045 SEESAETGSSSTF-----IKREDE-----TIE---DIDMDDIGIDSSDL-VED 1086

Qy 1104 SFL 1106  
Db 1087 SFL 1089

RESULT 12  
US-09-769-987-2  
Sequence 2, Application US/09769987  
Patent No. US20020055129A1  
GENERAL INFORMATION:  
APPLICANT: Matsui, Toshimitsu  
APPLICANT: Aaronson, Stuart A.  
TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor  
FILE REFERENCE: 14014.0266U2  
CURRENT APPLICATION NUMBER: US/09/769,987  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 08/460,656  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: US 08/439,095  
PRIOR FILING DATE: 1995-05-11  
PRIOR APPLICATION NUMBER: US 07/915,884  
PRIOR FILING DATE: 1992-07-20  
PRIOR APPLICATION NUMBER: US 07/308,282  
PRIOR FILING DATE: 1989-02-09  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 1089  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence; No. US20020055129A1 =  
US-09-769-987-2

Query Match 40.8%; Score 2351.5; DB 9; Length 1089;  
Best Local Similarity 44.0%; Pred. No. 6.4e-125;  
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;

Qy 8 PALALKEGELL-LSLALLEPQISQGLVTPPGPELVNVSSTFVLTCGSAFVWVE-RM 65  
Db 6 PAFVLGCLLTGSLILC---QLSLPSIL-PNENEKVQLNSFSRLRCFGESEVSWQYPM 61

Qy 66 SQPPQEM-----AKAQDGTSSVLTNLTLGDTGEYFCTHNSRGLTDT-ERKRLYIFV 120  
Db 62 SEESDSVIRNEENNSGLFVTVLEVSSASAHTGLTYCYNNHTQTEENELEGRHIYIV 121

Qy 121 PDPTVGLPNDABELFIFLITEITPCRTVDPQLVTLHEKKGDVALPVVDHORGFS 180



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Db 122 PDPVAFVFLGMDTVLIVEDDDSAIIPCRITDPTVTLHNSG--VVPASVDSRQGFN 179
Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSS--INVSVNAVQTVVRQGENITLMCIIVG 239
Db 180 GTFTVGVYICBATVKGKFTQIPFNVAALKATSELDLEMEALKTVYKSGETIVVTCVAFN 239
Qy 240 NDVVNEFWTPRKESGR--LVEPVTDPLDMPVHRSILHIPSAAELEDSTVTCNVTES 296
Db 240 NEVVDLQWTPGCVKGKGTMLBEIKVPSIKLVY----TLVTPATVKSDDGVECAARQA 295
Qy 297 VNDHQDEKAINITVYVESGYVRLGEGVTQFAELHRSRTILQVVFEPYPPPTVLMFKDNRT 356
Db 296 TREVKEMKVTISVHEKGFTIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPIPRISLWKNLT 355
Qy 357 LGDSSAGEIALSTRNVSETRYVSELTVLRVVAABAGHYTMRAFHEDAELVOLSQLQINVP 416
Db 356 LIENLT-EITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEADAVKSYTFELLTQVP 414
Qy 417 VRVLELSESHPDS-GEOTVRCRCRGMPPQNIILWSACRDLKRCRELPPPTLLGNS----- 469
Db 415 SSILDVDDHGGTGGGTVCRTAGETPLDIEWMICDKIKKNNETSWITLANNVNIIT 474
Qy 470 ---SEESQLETNVYVVEEPEWSTLRLQHVDRPLSVRCLTRNNAVGDQTOEVIIVVPH 526
Db 475 EIHSDRSTVEGRVTF-----AKVEETIAVRCLAKNLLGAENRELKLVP 519
Qy 527 SLPFKVVVISAILALVLTITSLIILIMLWQKPRYRIRKVIETSVSSDGEHYIYVDPMQ 586
Db 520 TLRSELTAAAVLVLVIVISLVLVWIKQPRYRIRWVIESIPDGEHYIYVDPMQ 579
Qy 587 LPYDSTWELPRDQLVGLRTLGSAFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQ 646
Db 580 LPYDSRWEPRDGLVLRVIGSAGFGVVEGTAGLSRSPQVWKVAVKMLKPTARSSEKQ 639
Qy 647 ALMSELKIMSHLGHPLNVLNLLGACTKGGPIIITEYCRYGDLVDYLHNRKHTFLOHSD 706
Db 640 ALMSELKIMTHLGHPLNVLNLLGACTKSGPIIITEYCRYGDLVDYLHNRKDSFSLHPE 699
Qy 707 KRPPPSAELYSNAL-PVGLPLPSHVSILTGESDGGYMDMSKDESVDVVPMLDMKGVKYAD 765
Db 700 K---PKELDI FGLNPADESTRSVILSFENNGDYMMDKQADTQYVPMLEKEVSKYSD 756
Qy 766 IESSNYMAPYDNTVPSAPERTCRATLINE-SPVLSYMDLVGFSGYQVANGMEFLASKNCVH 824
Db 757 IORSLYDRPAS YKKSKMLDSEVKNLSSDDNSEGLTLLDLSFTYQVARGNEFLASKNCVH 816
Qy 825 RDLAARNVLICEGLVKICDFGLARDIMRDSNVISKSTPLPKWMAPEISFNSLYTTL 884
Db 817 RDLAARNVLLAQQKIVKICDFGLARDIMHDSNVYSKSTPLPKWMAPEISFONLYTTL 876
Qy 885 DVMSFGILLWEIFTLGCTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMOKWEEK 944
Db 877 DVMSYIGILLWEIFTSLGCTPYPGMWVDSTFYNKIKSGYRMAKPDHATSEVTEIMVKWCNSE 936
Qy 945 FEIRPPFSQVLLLERLLGEGYKKYQQVDEEFLRSDHPAILRSQARLPFGHLSPLDT 1004
Db 937 PEKRPSPHYLSEIVENLPQYKYSYKIEIHLDFLKSHPAVARMR-----VDS 984
Qy 1005 SSVLYTAVQNE-----GNDYIITPL--DPKPEVADGGPLEGGSPLA 1045
Db 985 DNAYIGVYTKNEEDKLDMWEGGLDEQRLSDAGSYIIPLDIDPVPBEEDLKGKRNHSSQT 1044
Qy 1046 S---STLNEVNTSSTISCDSPLEPQDEPEPEPQLEOPEPEPELEQPLDSCCAPRAEAD 1103
Db 1045 SESATETGSSSTF-----IKREDE-----TIE-----DIDMDDDIDGSDSL-VED 1086
Qy 1104 SFL 1106
Db 1087 SFL 1089

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RESULT 13

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US-09-919-497-90
; Sequence 90, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-919-497-90

Query Match 40.8%; Score 2351.5; DB 9; Length 1089;
Best Local Similarity 44.0%; Pred. No. 6.4e-125;
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;

Qy 8 PALALKGEILL-LSLLLLEPQISQGLVVTTPPGPELVNLVSVSTFVLTCGSAFVWME-RM 65
Db 6 PAFVLVGLCLLTGLSLILC---QLSLPSIL-PNENKVVQLNSSFSLRCFCGESEVSWQYPM 61
Qy 66 SQPPQEM-----AKAQDGFSSVLTNLTGLDTGEYFCHNDSRGLETD-ERKRLYIFV 120
Db 62 SEESDVEIRNEENNSGLFVTVLEVSSAASAAHTGLTYCYNNHTQTEENLEGRHIYV 121
Qy 121 PDPVGFPLNDABEELFIFTEITPCRTVTDPLQVLVTLHEKKGDVALPVPVDHORGFS 180
Db 122 PDPVAFVFLGMDTVLIVEDDDSAIIPCRITDPTVTLHNSG--VVPASVDSRQGFN 179
Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSS--INVSVNAVQTVVRQGENITLMCIIVG 239
Db 180 GTFTVGVYICBATVKGKFTQIPFNVAALKATSELDLEMEALKTVYKSGETIVVTCVAFN 239
Qy 240 NDVVNEFWTPRKESGR--LVEPVTDPLDMPVHRSILHIPSAAELEDSTVTCNVTES 296
Db 240 NEVVDLQWTPGCVKGKGTMLBEIKVPSIKLVY----TLVTPATVKSDDGVECAARQA 295
Qy 297 VNDHQDEKAINITVYVESGYVRLGEGVTQFAELHRSRTILQVVFEPYPPPTVLMFKDNRT 356
Db 296 TREVKEMKVTISVHEKGFTIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPIPRISLWKNLT 355
Qy 357 LGDSSAGEIALSTRNVSETRYVSELTVLRVVAABAGHYTMRAFHEDAELVOLSQLQINVP 416
Db 356 LIENLT-EITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEADAVKSYTFELLTQVP 414
Qy 417 VRVLELSESHPDS-GEOTVRCRCRGMPPQNIILWSACRDLKRCRELPPPTLLGNS----- 469
Db 415 SSILDVDDHGGTGGGTVCRTAGETPLDIEWMICDKIKKNNETSWITLANNVNIIT 474
Qy 470 ---SEESQLETNVYVVEEPEWSTLRLQHVDRPLSVRCLTRNNAVGDQTOEVIIVVPH 526
Db 475 EIHSDRSTVEGRVTF-----AKVEETIAVRCLAKNLLGAENRELKLVP 519
Qy 527 SLPFKVVVISAILALVLTITSLIILIMLWQKPRYRIRKVIETSVSSDGEHYIYVDPMQ 586
Db 520 TLRSELTAAAVLVLVIVISLVLVWIKQPRYRIRWVIESIPDGEHYIYVDPMQ 579
Qy 587 LPYDSTWELPRDQLVGLRTLGSAFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQ 646
Db 580 LPYDSRWEPRDGLVLRVIGSAGFGVVEGTAGLSRSPQVWKVAVKMLKPTARSSEKQ 639
Qy 647 ALMSELKIMSHLGHPLNVLNLLGACTKGGPIIITEYCRYGDLVDYLHNRKHTFLOHSD 706
Db 640 ALMSELKIMTHLGHPLNVLNLLGACTKSGPIIITEYCRYGDLVDYLHNRKDSFSLHPE 699
Qy 707 KRPPPSAELYSNAL-PVGLPLPSHVSILTGESDGGYMDMSKDESVDVVPMLDMKGVKYAD 765

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Db 700 K---PKKELDIIFGLNPADESTRSYVILSFENNNDYMDKQADTTQVPMLEKESKYS 756  
 QY 766 IESSNMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824  
 Db 757 IQRSYDRPASYYKKSMLESEVQKLLSDNSEGTLTLLDLSFTYQVARGMEFLASKNCVH 816  
 QY 825 RDLAARNVLICBGLVKICDFGLARDIMRDSNYISKGSTFLPKWMAPEISFNLSYTLT 884  
 Db 817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPKWMAPEISFNLSYTLT 876  
 QY 885 DWSFGILLWEIFTLGTPPELPMNEQFYNATKRGYMAQPAHASEDEIYEMOKWEEK 944  
 Db 877 DWSYGILLWEIFSLGTPPGMMVDSTFYNKIKSGYMAKPDHATSEVYEVIMVKWNS 936  
 QY 945 FEIRPPFSQVLLERLLGEGYKKYQOVDDEEFLRSDHPAILRSQARLPFGHGLRSP 1004  
 Db 937 PEKRPFSYHLSEIVENLLPQYKSYEKIHLDFKSDHPAVARMR-----VDS 984  
 QY 1005 SSVLYTAVQNE-----GDNDYIILPL--DPKPEVADEGLEGSPLA 1045  
 Db 985 DNAYIGVYKNEEDKLDWEGGLEQRLSADSGYIILPLDIDPVPBEEDLGKRNHSSQT 1044  
 QY 1046 S---STINEVNTSITSCDSPLEPQDEPEPEPELOVEPEPELEQLPDSCCAPRAEAE 1103  
 Db 1045 SEESAIETGSSSTF-----IKREDE-----TIE-----DIDMDDIGIDSSDL-VED 1086  
 QY 1104 SFL 1106  
 Db 1087 SFL 1089  
 RESULT 14  
 US-09-866-510-2  
 ; Sequence 2, Application US/09866510  
 ; Patent No. US20020113041  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KAZLAUSKAS, ANDRIUS  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES  
 ; FILE REFERENCE: ERM-104.01  
 ; CURRENT APPLICATION NUMBER: US/09/866,510  
 ; PRIOR FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: 60/250,747  
 ; PRIOR FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: 60/289,103  
 ; PRIOR FILING DATE: 2001-05-07  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; TYPE: PRT  
 ; LENGTH: 1089  
 ; ORGANISM: Homo sapiens  
 ; US-09-866-510-2  
 Query Match 40.8%; Score 2351.5; DB 9; Length 1089;  
 Best Local Similarity 44.0%; Pred. No. 6.4e-125;  
 Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;  
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 Db 122 PDPDAVFLGMDTYLVIVEDDSSAIIPCTTDPETVTLHNSG--VVPASYSRQGFN 179  
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QY 240 NDVNFPEWTPRKESGR---LVEPVTFDFLDMPYHIRSILHPSAELESBGTYTCNVTS 296  
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 Db 1087 SFL 1089

RESULT 15  
 US-09-955-363-36  
 ; Sequence 36, Application US/09955363  
 ; Patent No. US20020173621A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sledziwski Ph.D., Andrzej Z  
 ; Bell, Lillian A.

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; Kingvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; FUSIONS
;
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/955,363
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELETYPE: 3723836
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
;
; US-09-955-363--36
;
; Query Match 40.8%; Score 2351.5; DB 9; Length 1089;
; Best Local Similarity 44.0%; Pred. No. 6.4e-125;
; Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;
;
; QY 8 PALALXGELL-LISLILLLEPOISQGLVTPPGPELVNVSSTFVLTCGSAAPVWE-RM 65
; DB 6 PAFVLVGLCLTGLSLILC---QLSLPSIL-PNENKVVQLNSSFSLRCFGESEVSWQYPM 61
; QY 66 SQEPPQEM---AKAQDGTFSVLTNLTLTGLDTGEVFCYTHNDSRGLETD-ERKRLYIFV 120
; DB 62 SEESDVEIRNENNSGLFVTVLEVSSASAHTGLYTCYNNHTQTEELEGRHIYIV 121
; QY 121 PDFTVGLPNDAELFIPLTEITIPCKRVTDPQLVLTILHEKKGDVALPVPYDHQGRFS 180
; DB 122 PDPDAFVPLGMDYLVIVEDDDSAIIPCRITDPTETPVLHNSG--VVPASYDSRQGFN 179
; QY 181 GIFEDRSYICKTIGREVSDSAYVYVRLQVSS-INVSNAVQTVVROGENITLMCIVIG 239
; DB 180 GTFTVGPYICEATVKGKFTQIPFNLYALKATSELDLEALKTVYKSGETIVVTCAVFN 239
; QY 240 NDVVFNEWTYPRKESGR--LVPEVTFDFLDMYHIRSIILHIPSAALEDSGTVTCNVTES 296
; DB 240 NEVVDLQWTPYGEVKGKGTILEIKVPSIKLY---TLTVEATVKSQGYECAARQA 295
; QY 297 VNDHQDEKAINITVWSSGYVRLIGVGTIQFABLHRSRTLLQVVFAYPPPTVLWFKDNRT 356
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; DB 415 SSILDVDDHGGSTGGQTVRCATAGTFLPDIEWMICDKIKCNCNETSWITLANNVSNIIIT 474
; QY 470 ---SEESOLETNVTYWEEBEQPEVVTSLRLQHVDRPLSVRCFLRNAVGQDTCQEVTVWPH 526
; DB 475 EHSRDRSTVEGRVTF-----AKVEETIAVRCLAKULLGAENRELKLVAP 519
; QY 527 SLFPKVVVISAILALVVLTIISLIILMLWQKPRYEIRKWKVIESVSDGHEYIYVDPMQ 586
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; QY 766 IESSNYMAPVDNVVPSAPERTCRATLINE-SPVLSTYMDLVGFSYOVANGMEFLASKNCVH 824
; DB 757 IQRSLYDRPASYYKKSMLDSEVKNLSDNSEGLTLDLLSFTYQVARGMEFLASKNCVH 816
; QY 825 RDLAARNVLICRGLVKICDFGLARDIMRDSNVISKGSTFLPLKMWAPESIFNSLYTTL 894
; DB 817 RDLAARNVLLAQCKIVKICDFGLARDIMHDSNVVSKGSTFLPVKMWAPESIFDNLYTTL 876
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; DB 877 DVWSYGILLWEIFSLGGTTPPGMMVDSTFYNKIKSGYRMAKPDHATSEYVEIMVKCWSE 936
; QY 945 FEIRPPFSOLVLLERLIGEGYKKYQVDEBFLRSDHPAILRQARLPGFHGLRSLPDT 1004
; DB 937 PEKRPSTYHLSEIVENLLPGQYKSYEKIHLDFLKSDFHFAVAMR-----VDS 984
; QY 1005 SSVLYTAVQPNE-----GDNDYIPLP--DPKPEVADGPLEGSPSLA 1045
; DB 985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLDIDPVPPEEDLGRNRRHSQT 1044
; QY 1046 S--STLNEVNTSSTSCDSPLEPQDEPEPEPQLEQVEPEPELEQLPGCGCAPRAEAD 1103
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; QY 1104 SFL 1106
; DB 1087 SFL 1089

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Job time : 78.0692 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2005, 07:10:35 ; Search time 32.2478 Seconds  
(without alignments)  
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Title: US-10-027-400-4  
Perfect score: 5766  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5766	100.0	1106	2	US-08-460-510-2
3	5766	100.0	1106	2	US-08-460-490-2
4	5766	100.0	1106	3	US-08-462-728-4
5	5766	100.0	1106	3	US-08-461-917-4
6	5766	100.0	1106	4	US-08-464-436-4
7	5766	100.0	1106	4	US-08-464-436-4
8	5766	100.0	1106	5	PCT-US92-00730-2
9	5766	100.0	1106	5	PCT-US92-00862-2
10	5762	99.9	1106	1	US-08-180-195-2
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12	5762	99.9	1106	2	US-08-475-458-2
13	5762	99.9	1106	3	US-08-980-400-2
14	5762	99.9	1106	3	US-09-583-459A-2
15	5762	99.9	1106	3	US-09-583-210-2
16	5762	99.9	1106	3	US-09-583-449A-2
17	5762	99.9	1106	3	US-09-435-059-2
18	5760	99.9	1106	4	US-09-866-510-22
19	5758	99.9	1106	4	US-09-866-510-16
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21	5756	99.8	1106	4	US-09-866-510-18
22	5756	98.4	1090	4	US-09-866-510-14
23	3076	53.3	668	4	US-09-949-016-8139
24	2882	50.0	581	4	US-09-866-510-24
25	2675.5	46.4	566	1	US-08-810-116-11
26	2675.5	46.4	566	2	US-07-930-548A-11
27	2352.5	40.8	1089	4	US-09-866-510-10

28	2351.5	40.8	1089	1	US-08-180-195-36	Sequence 36, Appl
29	2351.5	40.8	1089	1	US-08-168-917-4	Sequence 4, Appl
30	2351.5	40.8	1089	1	US-08-477-329-36	Sequence 36, Appl
31	2351.5	40.8	1089	2	US-08-475-458-36	Sequence 36, Appl
32	2351.5	40.8	1089	2	US-08-460-510-4	Sequence 4, Appl
33	2351.5	40.8	1089	2	US-08-460-490-4	Sequence 4, Appl
34	2351.5	40.8	1089	3	US-08-980-400-36	Sequence 36, Appl
35	2351.5	40.8	1089	3	US-08-462-728-2	Sequence 2, Appl
36	2351.5	40.8	1089	3	US-09-583-459A-36	Sequence 36, Appl
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38	2351.5	40.8	1089	3	US-09-583-449A-36	Sequence 36, Appl
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41	2351.5	40.8	1089	4	US-08-464-436-2	Sequence 2, Appl
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43	2351.5	40.8	1089	4	US-09-769-987-2	Sequence 2, Appl
44	2351.5	40.8	1089	4	US-09-866-510-2	Sequence 2, Appl
45	2351.5	40.8	1089	4	US-09-919-497-90	Sequence 90, Appl

ALIGNMENTS

RESULT 1  
US-08-168-917-2  
; Sequence 2, Application US/08168917  
; Patent No. 5686572  
; GENERAL INFORMATION:  
; APPLICANT: Wolf, David  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: Fretto, Larry J.  
; APPLICANT: Giese, Neill A.  
; APPLICANT: Escobedo, Jaime A.  
; APPLICANT: Williams, Lewis T.  
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND  
; STREET: Stuart Street Tower, 20th Floor \ One Market  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,917  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/650,793  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: 12418-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1106 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-168-917-2

Query Match 100.0%; Score 5766; DB 1; Length 1106;

Best Local Similarity 100.0%; Pred. No. 0;		Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Qy	481	TYWEEQEFVWSTRLQHVDRPLSVRCTLRNAGVQDQEVIVVPHSLPKVVI SAILA	540
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Db	841	KICDFGLARDIMDSYIISKGSTFLPLKWMAPSIIFNSLYTTLSDVWSEGILLWEITFLG	900
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Qy	961	LLGEGYKKYQVDEBFLRSDHPAILRSQARLPFGHLSPLDTSSVLYTAVQPNEGDND	1020
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RESULT 2  
 US-08-460-510-2  
 ; Sequence 2, Application US/08460510  
 ; Patent No. 5872218  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wolf, David  
 ; APPLICANT: Tomlinson, James E.  
 ; APPLICANT: Fretto, Larry J.  
 ; APPLICANT: Giese, Neill A.  
 ; APPLICANT: Escobedo, Jaime A.  
 ; APPLICANT: Williams, Lewis T.  
 ; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN  
 ; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: TOWNSEND and TOWNSEND and CREW  
 ; STREET: One Market Plaza, Steuart Street Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA: US/08/460,510  
 ; APPLICATION NUMBER: US/08/460,510  
 ; FILING DATE: 02-JUN-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dow, Karen B.  
 ; REGISTRATION NUMBER: 29,684  
 ; REFERENCE/DOCKET NUMBER: 012418-001430  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 326-2400  
 ; TELEFAX: (415) 326-2422  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1106 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-460-510-2

Query Match 100.0%; Score 5766; DB 2; Length 1106;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MRPGAMPALALGKELLSSLLLELPQISQGLVWTPPGPELVNVSSTFVLTCSSAPV 60  
 Db 1 MRPGAMPALALGKELLSSLLLELPQISQGLVWTPPGPELVNVSSTFVLTCSSAPV 60  
 Qy 61 VWRMSQEPPEQEMAKAQDGTFSVLTLNLTGLDGTGEYFCTHNSRGLTDERKRLYIFV 120  
 Db 61 VWRMSQEPPEQEMAKAQDGTFSVLTLNLTGLDGTGEYFCTHNSRGLTDERKRLYIFV 120  
 Qy 121 PDPVTGFLPNDAELFIFLITEITIPCRVTPDQLVTLHEKKGVALPVPYDHORGFS 180  
 Db 121 PDPVTGFLPNDAELFIFLITEITIPCRVTPDQLVTLHEKKGVALPVPYDHORGFS 180  
 Qy 181 GIFEDRSYICKTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIIGN 240  
 Db 181 GIFEDRSYICKTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIIGN 240  
 Qy 241 DVNFETYPRKSGRLVPEVTFLLDMPYHRSILHIPSAELEDSTGTYTCNVTESVNDH 300

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Db 241 DVNFEWTPKESGRIVEPTDPLDMPYHRSILHIPSABLEDSCTYTCNVTSVNDH 300
Qy 301 QDEKAINITVBSGYVRLGEGVTLQFAELHRSRTLQVFEAYPPPTVLMFKDNRITLGD 360
Db 301 QDEKAINITVBSGYVRLGEGVTLQFAELHRSRTLQVFEAYPPPTVLMFKDNRITLGD 360
Qy 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQQLINVPVRL 420
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQQLINVPVRL 420
Qy 421 ELSSEHPDSGEQTVRCGRGMPQPNIIWSACRDLKRCRPRELPTLLGNSSEESQLETNV 480
Db 421 ELSSEHPDSGEQTVRCGRGMPQPNIIWSACRDLKRCRPRELPTLLGNSSEESQLETNV 480
Qy 481 TYWEEQEPEFVSTLRQLHVDRLPLSVRCCTLRNAGVQDTQEVIVVPHSLPKVVISAILA 540
Db 481 TYWEEQEPEFVSTLRQLHVDRLPLSVRCCTLRNAGVQDTQEVIVVPHSLPKVVISAILA 540
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Db 541 LVVLTIIISLILMLQKPKRYEIRWKVIESVSDGHEIYIVDPMQLPYDSTWELPRDQL 600
Qy 601 VLGRITLGSAGFGQVVEATAGLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660
Db 601 VLGRITLGSAGFGQVVEATAGLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660
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Db 661 HLMNVNLGACTGGPIIYITECRYGDLVDYLHRNKHFTLQHSKRRPPSAELYSNAL 720
Qy 721 PVGLPLPSHVSLSGESDGYMDMSKDESVDYVPMKMGDKVYADIESSNYMAPYDNYVP 780
Db 721 PVGLPLPSHVSLSGESDGYMDMSKDESVDYVPMKMGDKVYADIESSNYMAPYDNYVP 780
Qy 781 SAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Db 781 SAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
Qy 841 KICDFGLARDIMRDSNYSKGSFTPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900
Db 841 KICDFGLARDIMRDSNYSKGSFTPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900
Qy 901 GTPYPELPMNEQFYNAIKRGYMAQPAHASDEIYEIMQKWEKFEIRPPFSQLVLLER 960
Db 901 GTPYPELPMNEQFYNAIKRGYMAQPAHASDEIYEIMQKWEKFEIRPPFSQLVLLER 960
Qy 961 LLEGYKKKYQVDEEPLRSDHPAILRSQARLPFGHGLRSPLDTSVSLYTAQVNEGND 1020
Db 961 LLEGYKKKYQVDEEPLRSDHPAILRSQARLPFGHGLRSPLDTSVSLYTAQVNEGND 1020
Qy 1021 YIPLPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLEQV 1080
Db 1021 YIPLPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPQDEPEPEPQLEQV 1080
Qy 1081 EPPELEQLPDSGCPAPRAEADSFL 1106
Db 1081 EPPELEQLPDSGCPAPRAEADSFL 1106
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## RESULT 3

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US-08-460-490-2
; Sequence 2, Application US/084604090
; Patent No. 5891652
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Pretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
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; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and CREW
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,490
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-490-2
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Query Match 100.0%; Score 5766; DB 2; Length 1106;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRLPGAMPALALAGELLLLSLLLSLSPQISQGLVVTTPGPELVNVSSTFVLTCSGAPV 60
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Db 61 VWRMSQEPPOEMAKADGTFSSVLTLTNLGTGDTGEYFCTHDSRGLTDERKRLYIFV 120
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Db 121 PDTVGLFPLNDABELFIFLITEITPCRVTPDQLVVTLHKKGDVALPVVDHQRGFS 180
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Db 181 GIFEDRSYICKTIGDREVDSDAYVYRLOVSSINVSNAVQTVVROGENITLMCIIGN 240
Qy 241 DVNFEWTPKESGRIVEPTDPLDMPYHRSILHIPSABLEDSCTYTCNVTSVNDH 300
Db 241 DVNFEWTPKESGRIVEPTDPLDMPYHRSILHIPSABLEDSCTYTCNVTSVNDH 300
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Db 301 QDEKAINITVBSGYVRLGEGVTLQFAELHRSRTLQVFEAYPPPTVLMFKDNRITLGD 360
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Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQQLINVPVRL 420
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Db 421 ELSSEHPDSGEQTVRCGRGMPQPNIIWSACRDLKRCRPRELPTLLGNSSEESQLETNV 480
Qy 481 TYWEEQEPEFVSTLRQLHVDRLPLSVRCCTLRNAGVQDTQEVIVVPHSLPKVVISAILA 540
Db 481 TYWEEQEPEFVSTLRQLHVDRLPLSVRCCTLRNAGVQDTQEVIVVPHSLPKVVISAILA 540
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Db 541 LVVLTIIISLIILMLQKKPYEIRWKVIESVSSDGHYIYVDMPQLPYDSTWELPRDQL 600  
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Db 841 KICDFGLARDIMRDSNYSKSTFLPLKMWAPESIFNSLYTTLSDVMSFGILLWEIETLG 900  
Qy 901 GTPYPELPMNEQFYNAIKRGYMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLVLLER 960  
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Db 961 LLGEGYKKYQOVDDEEFLRSDHPAILRSOARLPFGHLRSPDLTSSVLYTAVQNEGDND 1020  
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Db 1021 YIPLPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPODEPEPEPQLELOV 1080  
Qy 1081 EPPELEQLPDSGCPAPRAEASFL 1106  
Db 1081 EPPELEQLPDSGCPAPRAEASFL 1106

## RESULT 4

US-08-462-728-4  
; Sequence 4, Application US/08462728  
; Patent No. 6043211  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, Lewis T.  
; APPLICANT: ESCOBEDO, Jaime A.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; STREET: Townsend and Townsend and Crew  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/462,728  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/309,322  
; FILING DATE: 10-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/151,414  
; FILING DATE: 02-FEB-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.

; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 2307K-267-2-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/326-2400  
; TELEFAX: 415/326-2422  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1106 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-462-728-4

Query Match 100.0%; Score 5766; DB 3; Length 1106;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 181 GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240  
Qy 241 DVNPFWTYPRKESGRVPEVTFDLDMPYHISILHI PSAELEDSDGTYTCNVTESVNDH 300  
Db 241 DVNPFWTYPRKESGRVPEVTFDLDMPYHISILHI PSAELEDSDGTYTCNVTESVNDH 300  
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Qy 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTMRAFHEDAEVLQSFQQLINVPVRVL 420  
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTMRAFHEDAEVLQSFQQLINVPVRVL 420  
Qy 421 ELSSEHPDSGEQTVRCGRGMPQPNIIWSACRDLKRCPRLEPPTLLGNSSEESQLETNV 480  
Db 421 ELSSEHPDSGEQTVRCGRGMPQPNIIWSACRDLKRCPRLEPPTLLGNSSEESQLETNV 480  
Qy 481 TYWEEEQEFVSTLRQLQHVDRPLSVRCITLRNAVGDQTEQVIIVPHSLPKVWVISAIA 540  
Db 481 TYWEEEQEFVSTLRQLQHVDRPLSVRCITLRNAVGDQTEQVIIVPHSLPKVWVISAIA 540  
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Db 541 LVVLTIIISLIILMLQKKPYEIRWKVIESVSSDGHYIYVDMPQLPYDSTWELPRDQL 600  
Qy 601 VLGRITLGSAGPQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSLKMHLGP 660  
Db 601 VLGRITLGSAGPQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSLKMHLGP 660  
Qy 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHNRKHTFLOHSDKRRPPSAELYSNAL 720  
Db 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHNRKHTFLOHSDKRRPPSAELYSNAL 720  
Qy 721 PVGLPLPSHVSLSLTGESDGGYMDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAYDNYVP 780  
Db 721 PVGLPLPSHVSLSLTGESDGGYMDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAYDNYVP 780  
Qy 781 SAPERTCRATLINESPVLVSYMDLVGFYSQVANGMEFLASKNCVHRDLAARNVLIICEGLV 840  
Db 781 SAPERTCRATLINESPVLVSYMDLVGFYSQVANGMEFLASKNCVHRDLAARNVLIICEGLV 840

QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
DB 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLLVLLER 960  
DB 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLLVLLER 960  
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DB 961 LLGEGYKKYQVDEEFLRSDHDPAILRSQARLPFGFHLRSPLODTSVLYTAVQPNEGDND 1020  
QY 1021 YIIPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPODEPEPQLELQV 1080  
DB 1021 YIIPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPODEPEPQLELQV 1080  
QY 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106  
DB 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106

## RESULT 5

US-08-461-917-4  
; Sequence 4, Application US/08461917  
; Patent No. 6372438  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, Lewis T.  
; APPLICANT: ESCOBEDO, Jaime A.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market, Steuart Street Tower, 20th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,917  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/309,322  
; FILING DATE: 10-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/151,414  
; FILING DATE: 02-FEB-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,694  
; REFERENCE/DOCKET NUMBER: 2307K-267-2-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/326-2400  
; TELEFAX: 415/326-2422  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1106 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-461-917-4

Query Match 100.0%; Score 5766; DB 3; Length 1106;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRUPGAMPALAKGELLALLSLLLLBPQISQGLVVTTPGPELVNVSSTFVLTCGSAVP 60  
|||||

DB 1 MRUPGAMPALAKGELLALLSLLLLBPQISQGLVVTTPGPELVNVSSTFVLTCGSAVP 60  
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DB 181 GIFEDRSYCKTKTIGREVDSDAYVYVRLQVSSINVSNAVQTVRGENITLMCIIGN 240  
QY 241 DVNFWFTYPRKESGRILVEPVTDFLLDMPYHISILHIPSAELEDSTYTCNVTESVNDH 300  
DB 241 DVNFWFTYPRKESGRILVEPVTDFLLDMPYHISILHIPSAELEDSTYTCNVTESVNDH 300  
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DB 301 QDEKAINITVWESGYVRLLEGEVGTLOFAELHRSRTLOVFEAYPPPTVLMFKNRTLGDS 360  
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DB 361 SAGEIALSTRNSETRYVSELTLVRVKVABAGHYTMRAFHEDAEOVLSFOLQINVPVRVL 420  
QY 421 ELSSEHPDSGEOQTVRCGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480  
DB 421 ELSSEHPDSGEOQTVRCGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480  
QY 481 TYWEEEOPEFVWSTLRLOHVDRPLSVRCRTLNRNAVQDQTSVIIVPHSLPKVVISAILA 540  
DB 481 TYWEEEOPEFVWSTLRLOHVDRPLSVRCRTLNRNAVQDQTSVIIVPHSLPKVVISAILA 540  
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DB 601 VLGRITLGSAGFQVWEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSSELKIMSHLGP 660  
QY 661 HLNVNLLGACTKGPIIYITEYCRYGDLVDYLHRNKHTPLQHSKRRRPPSAELYSNAL 720  
DB 661 HLNVNLLGACTKGPIIYITEYCRYGDLVDYLHRNKHTPLQHSKRRRPPSAELYSNAL 720  
QY 721 PVGLPLPSHVSLTGESDGGYMDSKDESVDYVPMKMGDKVYADIESSNYMAPYDNYVP 780  
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DB 781 SAPERTCRATLINESPVLSDYVGFSGYOVANGMEFLASKNCVHRDLAARNVLICEGLV 840  
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DB 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
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QY 961 LLGEGYKKYQVDEEFLRSDHDPAILRSQARLPFGFHLRSPLODTSVLYTAVQPNEGDND 1020  
DB 961 LLGEGYKKYQVDEEFLRSDHDPAILRSQARLPFGFHLRSPLODTSVLYTAVQPNEGDND 1020  
QY 1021 YIIPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPODEPEPQLELQV 1080  
DB 1021 YIIPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPODEPEPQLELQV 1080  
QY 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106  
DB 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106

[illegible]



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,436  
FILING DATE: 05-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/309,322  
FILING DATE: 10-FEB-1989  
APPLICATION NUMBER: US 07/151,414  
FILING DATE: 02-FEB-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 2307K-267-2-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/326-2400  
TELEFAX: 415/326-2422  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-08-464-436-4

Query Match	100.0%	Score	5766;	DB	4;	Length	1106;
Best Local Similarity	100.0%;	Prod.	No.	0;			
Matches	1106;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1	MRLPCAMPALAKGELLILLSLLLELLEPOISQGLVTPPGPELVLNVSTFVLTCSGSAPV	60				
Db	1	MRLPCAMPALAKGELLILLSLLLELLEPOISQGLVTPPGPELVLNVSTFVLTCSGSAPV	60				
Qy	61	VWRMSQEPPOEMAQAQDGTSSVLTLTNLTLGLDTGEYFCTHNSRGLJETDERKRLYIFV	120				
Db	61	VWRMSQEPPOEMAQAQDGTSSVLTLTNLTLGLDTGEYFCTHNSRGLJETDERKRLYIFV	120				
Qy	121	PDPTVGLPNDABELFLTEITETITPCRVTDQOLVVLTHEKKGDNALVPYDQHRGFS	180				
Db	121	PDPTVGLPNDABELFLTEITETITPCRVTDQOLVVLTHEKKGDNALVPYDQHRGFS	180				
Qy	181	GIFEDRSYICKTTIGDREVDSDAYVYRVLQVSSINVSNAVQTVVROQENITLMCIVIGN	240				
Db	181	GIFEDRSYICKTTIGDREVDSDAYVYRVLQVSSINVSNAVQTVVROQENITLMCIVIGN	240				
Qy	241	DVNVFETWYPRKESGRLEVPVTDFLDMPYHIRSILHIPSAELEDSGTYTCNVTESVNDH	300				
Db	241	DVNVFETWYPRKESGRLEVPVTDFLDMPYHIRSILHIPSAELEDSGTYTCNVTESVNDH	300				
Qy	301	QDEKAINITVVEGSGVRLGVBGLTQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGDS	360				
Db	301	QDEKAINITVVEGSGVRLGVBGLTQFAELHRSRTLQVVFAYPPPTVLWFKDNRTLGDS	360				
Qy	361	SAGSIALSTRNVSETRYVSELTLLVRVKVAEAGHYTMRAFHEDAEVQLSFQIQINVPVRVL	420				
Db	361	SAGSIALSTRNVSETRYVSELTLLVRVKVAEAGHYTMRAFHEDAEVQLSFQIQINVPVRVL	420				
Qy	421	ELSESHPDGSEQTVRCRGRGHPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV	480				
Db	421	ELSESHPDGSEQTVRCRGRGHPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV	480				
Qy	481	TYWEEEOQFEVVSTLRLQHVDRPLSVRCTLRNAVQDQTQEVIVVPHSLPFKKVWISAILA	540				
Db	481	TYWEEEOQFEVVSTLRLQHVDRPLSVRCTLRNAVQDQTQEVIVVPHSLPFKKVWISAILA	540				
Qy	541	LVLVTIISLIILIMLWOKKPYEIRWKVIESVSSDGHEYIYVDPMLQPLDYDSTWELPRDQL	600				
Db	541	LVLVTIISLIILIMLWOKKPYEIRWKVIESVSSDGHEYIYVDPMLQPLDYDSTWELPRDQL	600				

~~RESULT 8~~

PC-US92-00730-2  
Sequence 2, Application PC/TUS9200730  
GENERAL INFORMATION:  
APPLICANT: Wolf, David  
APPLICANT: Tomlinson, James E.  
APPLICANT: Fretto, Larry J.  
APPLICANT: Giese, Neill A.  
APPLICANT: Escobedo, Jaime A.  
APPLICANT: Williams, Lewis T.  
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN  
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND AND TOWNSEND  
STREET: Stewart Street Tower, 20th Floor \ One Market  
STREET: Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/00730  
FILING DATE: 19920128  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: 12418-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400



121 PDPTVGLPNDABELFLTEITPCRVTPDQVLTILHEKKGVALPVVYDHRGFS 180  
 121 PDPTVGLPNDABELFLTEITPCRVTPDQVLTILHEKKGVALPVVYDHRGFS 180  
 181 GIFEDRSYICKTTIGREVSDAYVYVRLQVSSINVSNAVQTVVROGENITLMCIIGN 240  
 181 GIFEDRSYICKTTIGREVSDAYVYVRLQVSSINVSNAVQTVVROGENITLMCIIGN 240  
 241 DVNFEWTPRKSGRLVEPVTDFLLDMPVHRSILHI PSAELEDSTYTCNVTVSNDH 300  
 241 DVNFEWTPRKSGRLVEPVTDFLLDMPVHRSILHI PSAELEDSTYTCNVTVSNDH 300  
 301 QDEKAINITVESGYVLLGEVGTQFAELHRSRTLQVFEAYPPPTVLMFKNRTLGDS 360  
 301 QDEKAINITVESGYVLLGEVGTQFAELHRSRTLQVFEAYPPPTVLMFKNRTLGDS 360  
 361 SAGEIALSTRNVSETRVSELTIVRVKVAAGHYTMRAFHEDAVQLSFQIQLNVPVRL 420  
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 421 ELSHSDPDSGEQVRCRGWGPQNIISACRDLKRCRELPTLLGNSSEESQLESTNV 480  
 421 ELSHSDPDSGEQVRCRGWGPQNIISACRDLKRCRELPTLLGNSSEESQLESTNV 480  
 481 TYWEEQEFVWSTRLQHVDRPLSVRCTLNNAVGDQTEVIVVPHSLPKVWVISAILA 540  
 481 TYWEEQEFVWSTRLQHVDRPLSVRCTLNNAVGDQTEVIVVPHSLPKVWVISAILA 540  
 541 LVVLTIIISLILIMLQKPKRYEIRWKVIESVSDGHEIYVDPMLPYDSTWELPRDQL 600  
 541 LVVLTIIISLILIMLQKPKRYEIRWKVIESVSDGHEIYVDPMLPYDSTWELPRDQL 600  
 601 VLGRITLGSAGFQVVEATAGLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660  
 601 VLGRITLGSAGFQVVEATAGLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660  
 661 HLNVNLLGACTGGPIYIITEVCYRGDVLVDYLRNKHHTFLQHSKRRPPSAELYSNAL 720  
 661 HLNVNLLGACTGGPIYIITEVCYRGDVLVDYLRNKHHTFLQHSKRRPPSAELYSNAL 720  
 721 PVGLPLPSHVSITGESDGYMDMSKDESVDYVPMMDKMGDKVYADIESSNMAYPDNYVP 780  
 721 PVGLPLPSHVSITGESDGYMDMSKDESVDYVPMMDKMGDKVYADIESSNMAYPDNYVP 780  
 781 SAPERTCRATLINESPVLSTYMDLVGRSYQVANGMEFLASKNCVHRDLAARNVLICEGLV 840  
 781 SAPERTCRATLINESPVLSTYMDLVGRSYQVANGMEFLASKNCVHRDLAARNVLICEGLV 840  
 841 KICDFGLARDIMRDSNYISKGSTPLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
 841 KICDFGLARDIMRDSNYISKGSTPLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
 901 GTPYPELPMNEQFNALIKRGYMAQPAHASDEIYIEMQKWEKFEIRPPFSQVLLLER 960  
 901 GTPYPELPMNEQFNALIKRGYMAQPAHASDEIYIEMQKWEKFEIRPPFSQVLLLER 960  
 961 LLGEGYKKYQOVDDEEFLRSDHPAILRSQARLPGHGLRSPDLTSSVLYTAVQNEGDND 1020  
 961 LLGEGYKKYQOVDDEEFLRSDHPAILRSQARLPGHGLRSPDLTSSVLYTAVQNEGDND 1020  
 1021 YIIPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPODEPEPPQLEQV 1080  
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 1081 EPEPELQLPDSCGAPAPAEADSFL 1106  
 1081 EPEPELQLPDSCGAPAPAEADSFL 1106

RESULT 10

US-08-180-195-2

; Sequence 2, Application us/08180195

; Patent No. 5567584  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sledziewski Ph.D., Andrzej Z  
 ; APPLICANT: Bell, Lillian A.  
 ; APPLICANT: Kindvogel Ph.D., Wayne R.  
 ; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS  
 ; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE  
 ; NUMBER OF SEQUENCES: 36  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry  
 ; STREET: 6300 Columbia Center  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.24  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/180,195  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/634,510  
 ; FILING DATE:  
 ; APPLICATION NUMBER: US 07/146,877  
 ; FILING DATE: 22-JAN-1988  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/347,291  
 ; FILING DATE: 02-MAY-1989  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Maki J.D., David J.  
 ; REGISTRATION NUMBER: 31,392  
 ; REFERENCE/DOCKET NUMBER: 990008.446C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-622-4900  
 ; TELEFAX: 206-682-6031  
 ; TELEX: 3723836  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1106 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-180-195-2

Query Match 99.9%; Score 5762; DB 1; Length 1106;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MRLPGAMPALALGKGLLLSLILLLEPQISQGLVWTPPGPELVLVNVSSTFVLTCSGAPV 60  
 Db 1 MRLPGAMPALALGKGLLLSLILLLEPQISQGLVWTPPGPELVLVNVSSTFVLTCSGAPV 60  
 Qy 61 VWRMSQEPPEQMAKQDGTFFSVTLTNTLTGLDTGEYFCTHNDSCRLETDERKRLYIFV 120  
 Db 61 VWRMSQEPPEQMAKQDGTFFSVTLTNTLTGLDTGEYFCTHNDSCRLETDERKRLYIFV 120  
 Qy 121 PDPTVGLPNDABELFLTEITPCRVTPDQVLTILHEKKGVALPVVYDHRGFS 180  
 Db 121 PDPTVGLPNDABELFLTEITPCRVTPDQVLTILHEKKGVALPVVYDHRGFS 180  
 Qy 181 GIFEDRSYICKTTIGREVSDAYVYVRLQVSSINVSNAVQTVVROGENITLMCIIGN 240  
 Db 181 GIFEDRSYICKTTIGREVSDAYVYVRLQVSSINVSNAVQTVVROGENITLMCIIGN 240  
 Qy 241 DVNFEWTPRKSGRLVEPVTDFLLDMPVHRSILHI PSAELEDSTYTCNVTVSNDH 300  
 Db 241 EVNFEWTPRKSGRLVEPVTDFLLDMPVHRSILHI PSAELEDSTYTCNVTVSNDH 300

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QY 301 QDEKAINITVSEGYVALLGEVGTQFAELHRSRTLQVFEAYPPPTVLFKDNRTLGDS 360
DB 301 QDEKAINITVSEGYVALLGEVGTQFAELHRSRTLQVFEAYPPPTVLFKDNRTLGDS 360
QY 361 SAGEIALSTRNVSETRYVSELTLLVRVKVABAGHYTWFRAFHDAEVQLSFQQLNVPVRVL 420
DB 361 SAGEIALSTRNVSETRYVSELTLLVRVKVABAGHYTWFRAFHDAEVQLSFQQLNVPVRVL 420
QY 421 ELSSEHSDSGEQTVCRCRGMPQPNIIWSACRDLKRCPRPPTLLGNSEESQLETNV 480
DB 421 ELSSEHSDSGEQTVCRCRGMPQPNIIWSACRDLKRCPRPPTLLGNSEESQLETNV 480
QY 481 TYWEEQEFVSTLRQLQVDRPLSVRCRTLNRNAVQDQTEVIVVPHSLPKFVVVISAILA 540
DB 481 TYWEEQEFVSTLRQLQVDRPLSVRCRTLNRNAVQDQTEVIVVPHSLPKFVVVISAILA 540
QY 541 LVVLTIIISLIIILMLQKKPRYIRWKVIESVSDGHEIYYVDPMLPYDSTWELPRDQL 600
DB 541 LVVLTIIISLIIILMLQKKPRYIRWKVIESVSDGHEIYYVDPMLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSLKMHLGP 660
DB 601 VLGRITLGSAGFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSLKMHLGP 660
QY 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHNRKHTFLQHSKRRPPSAELYSNAL 720
DB 661 HLNVNLLGACTKGGPIYIIITEYCRYGDLVDYLHNRKHTFLQHSKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSLLGESDGGYMDSKDESVDYVPMKMGDKVYADIESSNMAYPDNYVP 780
DB 721 PVGLPLPSHVSLLGESDGGYMDSKDESVDYVPMKMGDKVYADIESSNMAYPDNYVP 780
QY 781 SAPERTCRATLINESPVLSDVGLVGFSGYQVANGMEFLASKNCVHRDLAARNVLI CEGKLV 840
DB 781 SAPERTCRATLINESPVLSDVGLVGFSGYQVANGMEFLASKNCVHRDLAARNVLI CEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSFTPLKWMAPESIFNSLYTTLSDVMSFGILLWEIPTLG 900
DB 841 KICDFGLARDIMRDSNYISKGSFTPLKWMAPESIFNSLYTTLSDVMSFGILLWEIPTLG 900
QY 901 GTYPPELPMNEQFNATIKRGYRAQPAHASDEIYEIMQKWEKFEIRPPFSQVILLER 960
DB 901 GTYPPELPMNEQFNATIKRGYRAQPAHASDEIYEIMQKWEKFEIRPPFSQVILLER 960
QY 961 LLGEGYKKYQQVDEEFLRSDHAILRSQARLPFGHGLRSPDLTSSVLYTAVQNEGDND 1020
DB 961 LLGEGYKKYQQVDEEFLRSDHAILRSQARLPFGHGLRSPDLTSSVLYTAVQNEGDND 1020
QY 1021 YIIPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPODEPEPEFQLELQV 1080
DB 1021 YIIPDPKPEVADEGLESPSLASSTLNEVNTSSTISCDSPLEPODEPEPEFQLELQV 1080
QY 1081 EPEPELQPLDSCGPAPRAEADSFL 1106
DB 1081 EPEPELQPLDSCGPAPRAEADSFL 1106

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RESULT 11

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US-08-477-329-2
; Sequence 2, Application US/08477329
; Patent No. 5750375
; GENERAL INFORMATION:
; APPLICANT: Sledziowski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

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; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-329-2

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Query Match 99.9%; Score 5762; DB 1; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLGAMPALALKEGELLISLLSLLLEPQISQGLVVTTPGPELVNVSSTVLTCSGAPV 60
DB 1 MRPLGAMPALALKEGELLISLLSLLLEPQISQGLVVTTPGPELVNVSSTVLTCSGAPV 60
QY 61 VWERMQEPOEAKAQCQGTFFSVLTNTLTGDTGCTFYFCTHNDSCGLEDEKRLYIFV 120
DB 61 VWERMQEPOEAKAQCQGTFFSVLTNTLTGDTGCTFYFCTHNDSCGLEDEKRLYIFV 120
QY 121 PDFTVGFPLNDABELFIFLITEITIPCRVTPDQLVVTTLHEKKGDVALPVPDQHORGF 180
DB 121 PDFTVGFPLNDABELFIFLITEITIPCRVTPDQLVVTTLHEKKGDVALPVPDQHORGF 180
QY 181 GIFEDRSYCKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVRQGENITLMCIIGN 240
DB 181 GIFEDRSYCKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVRQGENITLMCIIGN 240
QY 241 DVNPFMTYPRKESGRVLPVPTDPLDMPVHISILHIPSALIEDSGTYTCNVTESVNDH 300
DB 241 DVNPFMTYPRKESGRVLPVPTDPLDMPVHISILHIPSALIEDSGTYTCNVTESVNDH 300
QY 301 QDEKAINITVSEGYVALLGEVGTQFAELHRSRTLQVFEAYPPPTVLFKDNRTLGDS 360
DB 301 QDEKAINITVSEGYVALLGEVGTQFAELHRSRTLQVFEAYPPPTVLFKDNRTLGDS 360
QY 361 SAGEIALSTRNVSETRYVSELTLLVRVKVABAGHYTWFRAFHDAEVQLSFQQLNVPVRVL 420
DB 361 SAGEIALSTRNVSETRYVSELTLLVRVKVABAGHYTWFRAFHDAEVQLSFQQLNVPVRVL 420
QY 421 ELSSEHSDSGEQTVCRCRGMPQPNIIWSACRDLKRCPRPPTLLGNSEESQLETNV 480
DB 421 ELSSEHSDSGEQTVCRCRGMPQPNIIWSACRDLKRCPRPPTLLGNSEESQLETNV 480
QY 481 TYWEEQEFVSTLRQLQVDRPLSVRCRTLNRNAVQDQTEVIVVPHSLPKFVVVISAILA 540
DB 481 TYWEEQEFVSTLRQLQVDRPLSVRCRTLNRNAVQDQTEVIVVPHSLPKFVVVISAILA 540
QY 541 LVVLTIIISLIIILMLQKKPRYIRWKVIESVSDGHEIYYVDPMLPYDSTWELPRDQL 600
DB 541 LVVLTIIISLIIILMLQKKPRYIRWKVIESVSDGHEIYYVDPMLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSLKMHLGP 660
DB 601 VLGRITLGSAGFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSLKMHLGP 660

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Db 961 LLGEGYKKYQVDEEFLRSDHPAILRSQARLPQFHLGRSLDTSVLYITAVQNEGDND 1020

Qy 1021 YIIPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEQDEPEPQLELQV 1080

Db 1021 YIIPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEQDEPEPQLELQV 1080

Qy 1081 EPEPEQLPDSGCPAPRAEADSFL 1106

Db 1081 EPEPEQLPDSGCPAPRAEADSFL 1106

RESULT 13

US-08-980-400-2

; Sequence 2, Application US/08980400

; Patent No. 6018026

; GENERAL INFORMATION:

; APPLICANT: Sledziwski Ph.D., Andrzej Z

; APPLICANT: Bell, Lillian A.

; APPLICANT: Kindsvogel Ph.D., Wayne R.

; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; FILING DATE: US/08/980,400

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/477,329

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 990008.446C6

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-622-4900

; TELEFAX: 206-682-6031

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1106 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-980-400-2

Query Match 99.98; Score 5762; DB 3; Length 1106;

Best Local Similarity 99.98; Pred. No. 0;

Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRLPGAMPALAKGELLLSLLLELLEPQISQGLVVTTPPGPELVNVSSTFVLTCGSAVP 60

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Db 61 WERMSPQEPQEMAKAQDGFSSVLTNLTGLDTGEYFCTHNDSRGLTDERKRLYIFV 120

Qy 121 PDPTVGLPNDARELFLTEITETITPCRVTPDQLVVTLHEKKGDVALPVPVDHQRGFS 180

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Db 181 GIFEDRSYICKTTIGDREVDSDAYYYVRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240

Qy 241 DVVNFWTYPRKESGRVLFVPTDFLLDMPYHRSILHIHPSAELEDSGTTCNVTESVNDH 300

Db 241 EVVNFWTYPRKESGRVLFVPTDFLLDMPYHRSILHIHPSAELEDSGTTCNVTESVNDH 300

Qy 301 ODEKAINITVRESGVRLAGEVCTLOFAELHRSRTLOVVFAYPPPTVLFKDNRTLGDS 360

Db 301 ODEKAINITVRESGVRLAGEVCTLOFAELHRSRTLOVVFAYPPPTVLFKDNRTLGDS 360

Qy 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQLOINVPVRL 420

Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQLOINVPVRL 420

Qy 421 ELSHSDSGEQTVCRCRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETVN 480

Db 421 ELSHSDSGEQTVCRCRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETVN 480

Qy 481 TYWEEEOEFVWSTLRLOHVDRPLSVRCITLRNAVGDQTOEVIIVPHSLPKVVIISAILA 540

Db 481 TYWEEEOEFVWSTLRLOHVDRPLSVRCITLRNAVGDQTOEVIIVPHSLPKVVIISAILA 540

Qy 541 LVVLTIIISIIILIMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMQLPYDSTWELPRDQ 600

Db 541 LVVLTIIISIIILIMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMQLPYDSTWELPRDQ 600

Qy 601 VLGRITLGSAGFQGVVEATAGHLSHQAATMKVAVKMLKSTARSSEKQALMSELKIMHSLGP 660

Db 601 VLGRITLGSAGFQGVVEATAGHLSHQAATMKVAVKMLKSTARSSEKQALMSELKIMHSLGP 660

Qy 661 HLNVNLLGACTKGPIIITTEYCRYGLDVLVLRNKHFTLOHHSKRRPPSAELYSNAL 720

Db 661 HLNVNLLGACTKGPIIITTEYCRYGLDVLVLRNKHFTLOHHSKRRPPSAELYSNAL 720

Qy 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMPLDMKGDVYADIESSNYMAPYDNYVP 780

Db 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMPLDMKGDVYADIESSNYMAPYDNYVP 780

Qy 781 SAPERTCRATLINESPVSLVMDLVGSYQVANGMEFLASKNCVHRDLAARNVLI CSGLV 840

Db 781 SAPERTCRATLINESPVSLVMDLVGSYQVANGMEFLASKNCVHRDLAARNVLI CSGLV 840

Qy 841 KICDFGLARDIMRDSNYISKGSTFFLPKWPAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900

Db 841 KICDFGLARDIMRDSNYISKGSTFFLPKWPAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900

Qy 901 GTPYPELPWNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLILLER 960

Db 901 GTPYPELPWNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLILLER 960

Qy 961 LLGEGYKKYQVDEEFLRSDHPAILRSQARLPQFHLGRSLDTSVLYITAVQNEGDND 1020

Db 961 LLGEGYKKYQVDEEFLRSDHPAILRSQARLPQFHLGRSLDTSVLYITAVQNEGDND 1020

Qy 1021 YIIPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEQDEPEPQLELQV 1080

Db 1021 YIIPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEQDEPEPQLELQV 1080

Qy 1081 EPEPEQLPDSGCPAPRAEADSFL 1106

Db 1081 EPEPEQLPDSGCPAPRAEADSFL 1106

RESULT 14

US-09-583-459A-2

; Sequence 2, Application US/09583459A

; Patent No. 6291212

; GENERAL INFORMATION:

; APPLICANT: Sledziwski Ph.D., Andrzej Z

; APPLICANT: Bell, Lillian A.

; APPLICANT: Kindsvogel Ph.D., Wayne R.

; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS

;; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE

;; TITLE OF INVENTION: FUSIONS

;; NUMBER OF SEQUENCES: 36

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Seed and Berry

;; STREET: 6300 Columbia Center

;; CITY: Seattle

;; STATE: WA

;; COUNTRY: USA

;; ZIP: 98104-7092

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.24

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/583,459A

;; FILING DATE: 30-MAY-2000

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/634,510

;; FILING DATE: 27-DEC-1990

;; APPLICATION NUMBER: US 07/146,877

;; FILING DATE: 22-JAN-1988

;; APPLICATION NUMBER: US 07/347,291

;; FILING DATE: 02-MAY-1989

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Maki J. David J.

;; REGISTRATION NUMBER: 31,392

;; REFERENCE/DOCKET NUMBER: 990008.446C3

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 206-622-4900

;; TELEFAX: 206-682-6031

;; TELEX: 3723836

;; INFORMATION FOR SEQ ID NO: 2:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 1106 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-09-583-459A-2

Query Match 99.9%; Score 5762; DB 3; Length 1106;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRLPGAMPALALKGELLLLSLLLLLEPQISQGLVVTTPPGPELVNVSVSTFVLTCSGAPV	60
Db	1	MRLPGAMPALALKGELLLLSLLLLLEPQISQGLVVTTPPGPELVNVSVSTFVLTCSGAPV	60
Qy	61	VWRMSQEPQEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNDSRGLETDERKRLYIFV	120
Db	61	VWRMSQEPQEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNDSRGLETDERKRLYIFV	120
Qy	121	PDPTVGLPNDAELFIFLFEITEITPCRVTPDQLVVTTLHEKKGVDVALPVPYDHQGF	180
Db	121	PDPTVGLPNDAELFIFLFEITEITPCRVTPDQLVVTTLHEKKGVDVALPVPYDHQGF	180
Qy	181	GIFEDRSYIKTTIGREVSDAYVYRQVSSINVSNAVQTVRQGENITLMCIIGN	240
Db	181	GIFEDRSYIKTTIGREVSDAYVYRQVSSINVSNAVQTVRQGENITLMCIIGN	240
Qy	241	DVNVFEWTPKSGRLVPEVTPDPLDMPYHISILHIPSAELEDSTYTCNVTVSNDH	300
Db	241	DVNVFEWTPKSGRLVPEVTPDPLDMPYHISILHIPSAELEDSTYTCNVTVSNDH	300
Qy	301	QDEKAINITVSGYVRLLEGEVGTLPFAELHRSRTLQVFEAYPPPTVLFKDNRTLGDS	360
Db	301	QDEKAINITVSGYVRLLEGEVGTLPFAELHRSRTLQVFEAYPPPTVLFKDNRTLGDS	360
Qy	361	SAGEIALSTRNVSETRYVSELTLVRKVAAGHYTMRAFHEDAEVQLSFQQLQINVPVRVL	420
Db	361	SAGEIALSTRNVSETRYVSELTLVRKVAAGHYTMRAFHEDAEVQLSFQQLQINVPVRVL	420

Qy	421	ELSESHPDGSEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN	480
Db	421	ELSESHPDGSEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN	480
Qy	481	TYWEEEOBEFVSTLRQLQVDRPLSVRCITLRNAVQDQTBQVIVVPHSLPKVVISAILA	540
Db	481	TYWEEEOBEFVSTLRQLQVDRPLSVRCITLRNAVQDQTBQVIVVPHSLPKVVISAILA	540
Qy	541	LVLVTIISLIIILIMLWQKKPRYBIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL	600
Db	541	LVLVTIISLIIILIMLWQKKPRYBIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL	600
Qy	601	VLGRTLGSAFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP	660
Db	601	VLGRTLGSAFGQVVEATAGHLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP	660
Qy	661	HLNVNLLGACTKGGPIIITEYCRYGDLVDYLHRNKHTFLQHSKRRRPPSAELYSNAL	720
Db	661	HLNVNLLGACTKGGPIIITEYCRYGDLVDYLHRNKHTFLQHSKRRRPPSAELYSNAL	720
Qy	721	PVGLPLPSHVSLSGTSGDGMDSKDESVDYVPMKMGDKYADIESSNYMAPYDNYVP	780
Db	721	PVGLPLPSHVSLSGTSGDGMDSKDESVDYVPMKMGDKYADIESSNYMAPYDNYVP	780
Qy	781	SAPERTCRATLINESPVLSTYMDLVGFYSQVANGMEFLASKNCVHRDLAARNVLI	840
Db	781	SAPERTCRATLINESPVLSTYMDLVGFYSQVANGMEFLASKNCVHRDLAARNVLI	840
Qy	841	KICDFGLARDIMRDSNYISKGSTFLPLKWPAPESIFNSLYTTLSDVMSFGILLWEIFTLG	900
Db	841	KICDFGLARDIMRDSNYISKGSTFLPLKWPAPESIFNSLYTTLSDVMSFGILLWEIFTLG	900
Qy	901	GTPYPELPWNEQFYNAIKGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLVLLER	960
Db	901	GTPYPELPWNEQFYNAIKGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLVLLER	960
Qy	961	LLGEGYKKYQQVDEEFRLSRDHPAILRSQARLPFGHLSPLDTSVLYTAVQFNEGDND	1020
Db	961	LLGEGYKKYQQVDEEFRLSRDHPAILRSQARLPFGHLSPLDTSVLYTAVQFNEGDND	1020
Qy	1021	YIIPDPKPPEVADEGPLEGSPSLASTNLNEVNTSTISCDSPLEPQDEPEPQLEQV	1080
Db	1021	YIIPDPKPPEVADEGPLEGSPSLASTNLNEVNTSTISCDSPLEPQDEPEPQLEQV	1080
Qy	1081	EPEPELEQLPDSGCPAPRAEADSFL	1106
Db	1081	EPEPELEQLPDSGCPAPRAEADSFL	1106

RESULT 15

US-09-583-210-2

; Sequence 2, Application US/09583210

; Patent No. 6291646

; GENERAL INFORMATION:

; APPLICANT: Sledziwski Ph.D., Andrzej Z

; APPLICANT: Bell, Lillian A.

; APPLICANT: Kindvogel Ph.D., Wayne R.

; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS

; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE

; TITLE OF INVENTION: FUSIONS

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry

; STREET: 6300 Columbia Center

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583,210
; FILING DATE: 30-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: 27-DEC-1990
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-583-210-2

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Query Match          99.9%; Score 5762; DB 3; Length 1106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLLGAMPALAKGELLSSLLLELLEPQISQGLVVTTPPGPELVNVSSTFVLTCSSAPV 60
DB 1 MRLLGAMPALAKGELLSSLLLELLEPQISQGLVVTTPPGPELVNVSSTFVLTCSSAPV 60
QY 61 VWERMSQEPQEMAKAQDGFSSVLTNLTLTGLDTGEYFCTHNDSSRGLTDERKRLYIFV 120
DB 61 VWERMSQEPQEMAKAQDGFSSVLTNLTLTGLDTGEYFCTHNDSSRGLTDERKRLYIFV 120
QY 121 PDPTVGFLPNDABELFLTEITITPCRVTPDQLVVTLHEKKGDVALPVPYDHOGRFS 180
DB 121 PDPTVGFLPNDABELFLTEITITPCRVTPDQLVVTLHEKKGDVALPVPYDHOGRFS 180
QY 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVROGENITLVCIVGN 240
DB 181 GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVROGENITLVCIVGN 240
QY 241 DVNFEWTPRKESGRLEVPVDFLLDMPYHRSILHIPSAELEDSTGYTCNVTESVNDH 300
DB 241 EVNFEWTPRKESGRLEVPVDFLLDMPYHRSILHIPSAELEDSTGYTCNVTESVNDH 300
QY 301 QDEKAINITVVGSGYVRLLEVGTLQFAELHRSRTLOVFEAYPPPTVLWFKNRTLGD 360
DB 301 QDEKAINITVVGSGYVRLLEVGTLQFAELHRSRTLOVFEAYPPPTVLWFKNRTLGD 360
QY 361 SAGEIALSTRNVSTRVVSSELTIVRVKVAEGHYTWEAFHEDAEVQLSFOLQINVPVRL 420
DB 361 SAGEIALSTRNVSTRVVSSELTIVRVKVAEGHYTWEAFHEDAEVQLSFOLQINVPVRL 420
QY 421 ELSSEHPDSGEQTVRCGRGMPQNI IWSACRDLKRCFRELPTLLGNSSEESQLETNV 480
DB 421 ELSSEHPDSGEQTVRCGRGMPQNI IWSACRDLKRCFRELPTLLGNSSEESQLETNV 480
QY 481 TYWEEQEFVWSTRLQHVDRPLSVRCCTLRNAVQDQTEVIVVPHSLPFXVVISAILA 540
DB 481 TYWEEQEFVWSTRLQHVDRPLSVRCCTLRNAVQDQTEVIVVPHSLPFXVVISAILA 540
QY 541 LVLTITLSLILIMLWOKKPYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600
DB 541 LVLTITLSLILIMLWOKKPYEIRWKVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600
QY 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660

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Search completed: March 11, 2005, 07:50:32  
Job time : 37.2478 secs

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DB 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660
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DB 661 HLNVNLLGACTKGPIIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720
QY 721 PVGLPLPSHVSITGESDGGYMDMSKDESVDYVPMIDMKGDVKYADIESSNYMAPYDNYVP 780
DB 721 PVGLPLPSHVSITGESDGGYMDMSKDESVDYVPMIDMKGDVKYADIESSNYMAPYDNYVP 780
QY 781 SAPERTCRATLINESPVLSTMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
DB 781 SAPERTCRATLINESPVLSTMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDYWSFGILLWEIFTLG 900
DB 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDYWSFGILLWEIFTLG 900
QY 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSOLVLLER 960
DB 901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSOLVLLER 960
QY 961 LLGEGYKKYQQVDEEFLRSHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
DB 961 LLGEGYKKYQQVDEEFLRSHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020
QY 1021 YIITPLDPKPEVADEGLESPSLASTLNEVNTSSTISCDSPLEQDEPEPEPQLELOV 1080
DB 1021 YIITPLDPKPEVADEGLESPSLASTLNEVNTSSTISCDSPLEQDEPEPEPQLELOV 1080
QY 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
DB 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2005, 04:13:19 ; Search time 129.495 Seconds  
(without alignments)  
3303.265 Million cell updates/sec

Title: US-10-027-400-4

Perfect score: 5766

Sequence: 1 MRLPGAMPALALKEGELLSS.....EQLPDSCGCPAPRAEDSFL 1106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5762	99.9	1106	1 AAP90127	Aap90127 Platelet
2	5762	99.9	1106	2 AAR99690	Aar99690 Platelet
3	5762	99.9	1106	6 ABP96311	Abp96311 Human pla
4	5762	99.9	1106	7 ABR84719	Abr84719 Human kin
5	5762	99.9	1106	7 ADF45082	Adf45082 Human kin
6	5762	99.9	1106	8 ABO84679	Abob84679 Human can
7	5760	99.9	1106	6 ABG72459	Abg72459 Human pla
8	5759	99.9	1106	2 AAR26205	Aar26205 Type B hu
9	5758	99.9	1106	6 ABG72456	Abg72456 Human pla
10	5757	99.8	1106	6 ABG72458	Abg72458 Human pla
11	5756	99.8	1106	6 ABG72457	Abg72457 Human pla
12	5745.5	99.6	1107	8 ABO84677	Abob84677 Human can
13	5691	98.7	1106	1 AAP90646	Aap90646 Human pla
14	5676	98.4	1090	6 ABG72455	Abg72455 Human pla
15	5657.5	98.1	1089	4 ABG20753	Abg20753 Novel hum
16	4975	86.3	1098	8 ABO84676	Abob84676 Mouse can
17	4972	86.2	1098	5 ABB57338	Abb57338 Mouse isc
18	4857.5	84.2	1158	8 ABO84675	Abob84675 Mouse can
19	4626	80.2	2129	4 ABG15478	Abg15478 Novel hum
20	4626	80.2	2129	4 ABG20749	Abg20749 Novel hum
21	2882	50.0	561	6 ABG72460	Abg72460 Human pla
22	2796.5	48.5	821	2 AAY28935	Aay28935 Platelet
23	2352.5	40.8	1089	6 ABG72453	Abg72453 Human pla
24	2351.5	40.8	1089	5 AAU84300	Aau84300 Human end
25	2351.5	40.8	1089	6 ABG72449	Abg72449 Human pla

# ALIGNMENTS

RESULT 1  
AAP90127  
ID AAP90127 standard; protein; 1106 AA.

XX AAP90127;  
AC AC  
XX  
DT 25-MAR-2003 (revised)  
DT 01-NOV-1989 (first entry)  
XX  
DE Platelet derived growth factor receptor.

XX Platelet derived growth factor receptor; human;  
KW ligand binding receptor analogues; isoforms; assays; antibodies;  
KW atherosclerosis; wound healing; peptide dimer; cDNA.

XX Homo sapiens.  
XX EP325224-A.  
XX  
PD 26-JUL-1989.  
XX  
PF 18-JAN-1989; 89EP-00100787.

XX 22-JAN-1988; 88US-00146877.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Siedziwesk AZ, Bell LA, Kindsvogel WR;  
XX WPI; 1989-214434/30.  
DR N-PSDB; AAN90355.

XX Secretd ligand-binding receptor analogues e.g. PDGF receptor - used in assays, in purifications and as or with therapeutic agents.  
XX Claim 2; Fig 1; 45pp; English.

XX Platelet derived growth factor receptor (see corresp. AAN90355). Used in the invention to make analogues that are secreted (pref. Ile-29 - Met-441, and Ile-29 - Lys-531; see specification for details). These analogues are easily purified, produced in large quantities recombinantly, used to produce antibodies, to screen ligands as imaging agents, as (ant-)agonists, or therapeutically for atherosclerosis and wound healing, and assays. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 1106 AA;

Query Match 99.9%; Score 5762; DB 1; Length 1106;

		Best Local Similarity 99.9%; Pred. No. 0;				Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MRLPGAMPALAKGELLISLLSLLLELPQISQGLVTPPGPELVNVSSTFVLTCSSAPV	60						
Db	1	MRLPGAMPALAKGELLISLLSLLLELPQISQGLVTPPGPELVNVSSTFVLTCSSAPV	60						
QY	61	VNERMSQEPPOEMAKAQDGTFFSVLTTLNLTGLDTGEYFCTHNSRGLTDERKRLYIFV	120						
Db	61	VNERMSQEPPOEMAKAQDGTFFSVLTTLNLTGLDTGEYFCTHNSRGLTDERKRLYIFV	120						
QY	121	PDPVTGFLPNDABELFIFLITEITIPCRVTDLPQVLVTLHKKGGVALPVPYDHQRGFS	180						
Db	121	PDPVTGFLPNDABELFIFLITEITIPCRVTDLPQVLVTLHKKGGVALPVPYDHQRGFS	180						
QY	181	GIFEDRSYICKTTIGDREVDSDAYVYRLOVSSINVSNAVTVROGENITLMCIVGN	240						
Db	181	GIFEDRSYICKTTIGDREVDSDAYVYRLOVSSINVSNAVTVROGENITLMCIVGN	240						
QY	241	DVNVFENTYPRKESGRLEVPVTDFLDMPYHRSILHIPSABLESDGTYTCNVTSVNDH	300						
Db	241	DVNVFENTYPRKESGRLEVPVTDFLDMPYHRSILHIPSABLESDGTYTCNVTSVNDH	300						
QY	301	ODEKAINITVBSGYVRLLEGEVGTQFAELHRSRTLQVVFAYPPPTVLMFKDNRTLGDS	360						
Db	301	ODEKAINITVBSGYVRLLEGEVGTQFAELHRSRTLQVVFAYPPPTVLMFKDNRTLGDS	360						
QY	361	SAGETALSRNVSERYSELTFLVRKVAAEAGHYTMRAFHEDAEOVLSFQLOINVPVRL	420						
Db	361	SAGETALSRNVSERYSELTFLVRKVAAEAGHYTMRAFHEDAEOVLSFQLOINVPVRL	420						
QY	421	ELSEHPDSGEOTVRCRGMPQNPNIISACRDLKRCPRELPTLLGNSSEESOLETNV	480						
Db	421	ELSEHPDSGEOTVRCRGMPQNPNIISACRDLKRCPRELPTLLGNSSEESOLETNV	480						
QY	481	TYWEEQEPEVSTLRLQHVDRPLSVRCITLRNAVQDQTOEVIIVPHSLPFWVVISAILA	540						
Db	481	TYWEEQEPEVSTLRLQHVDRPLSVRCITLRNAVQDQTOEVIIVPHSLPFWVVISAILA	540						
QY	541	LVLVTIISLILMLWQKPRYERIKWVIESVSSDGHYIYVDPMLPYDSTWELPRDOL	600						
Db	541	LVLVTIISLILMLWQKPRYERIKWVIESVSSDGHYIYVDPMLPYDSTWELPRDOL	600						
QY	601	VLGRTLGSAGFQVVEATAGLSHSQATMKVAVQMLKSTARSEKQALMSLKIMSHLGP	660						
Db	601	VLGRTLGSAGFQVVEATAGLSHSQATMKVAVQMLKSTARSEKQALMSLKIMSHLGP	660						
QY	661	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAEALYSNAL	720						
Db	661	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAEALYSNAL	720						
QY	721	PVGLPLPSSHVSLTGSDGGYMDMSKDESVDYVPMIDMKDGVKYADTESNNYMAPYDNYVP	780						
Db	721	PVGLPLPSSHVSLTGSDGGYMDMSKDESVDYVPMIDMKDGVKYADTESNNYMAPYDNYVP	780						
QY	781	SAPERTCRATLINESVLMIDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICGKLV	840						
Db	781	SAPERTCRATLINESVLMIDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICGKLV	840						
QY	841	KICDFGLARDIMRDSNYSIKSGSTFPLKWPAPESIFNSLYTLSDVWVSFGILLWEIFTLG	900						
Db	841	KICDFGLARDIMRDSNYSIKSGSTFPLKWPAPESIFNSLYTLSDVWVSFGILLWEIFTLG	900						
QY	901	GTYPPELPWNEQPYNAIKGYRMAQPAHASDEIYETMQCKWEKFEIRPPFSQVLULLER	960						
Db	901	GTYPPELPWNEQPYNAIKGYRMAQPAHASDEIYETMQCKWEKFEIRPPFSQVLULLER	960						
QY	961	LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPFGHLSPLDTSVLYTAVQPNEGDND	1020						
Db	961	LLGEGYKKYQQVDEEFLRSDHPAILRSQARLPFGHLSPLDTSVLYTAVQPNEGDND	1020						
QY	1021	YIIPLPDPKPEVADGEPLEGSPSLASSTINEVNTSTISCDSPLEPQDEPEPEPQLEQV	1080						
Db	1021	YIIPLPDPKPEVADGEPLEGSPSLASSTINEVNTSTISCDSPLEPQDEPEPEPQLEQV	1080						

Query Match 99.9%; Score 5762; DB 2; Length 1106;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPGAMPALAKGELLISLLSLLLELPQISQGLVTPPGPELVNVSSTFVLTCSSAPV 60  
 Db 1 MRLPGAMPALAKGELLISLLSLLLELPQISQGLVTPPGPELVNVSSTFVLTCSSAPV 60  
 QY 61 VNERMSQEPPOEMAKAQDGTFFSVLTTLNLTGLDTGEYFCTHNSRGLTDERKRLYIFV 120  
 Db 61 VNERMSQEPPOEMAKAQDGTFFSVLTTLNLTGLDTGEYFCTHNSRGLTDERKRLYIFV 120  
 QY 121 PDPVTGFLPNDABELFIFLITEITIPCRVTDLPQVLVTLHKKGGVALPVPYDHQRGFS 180

Sequence 1106 AA;  
 Disclosure; Fig 1; 45pp; English.  
 The amino acid sequence (AAR99690) of human platelet-derived growth factor receptor (PDGF-R) was deduced from a cDNA clone (AAT34552) isolated from a human diploid dermal fibroblast library. The cDNA can be used in novel constructs that allow the prodn. of secreted biologically active PDGF-R analogues. This may comprise linking a sequence coding for PDGF-R, or the ligand-binding domain of the PDGF-R extracellular region, to a protein secretion signal (e.g. SUC2) and promoter, and expression in transformed host cells, esp. Saccharomyces cerevisiae. The secreted PDGF-R analogues are used in ligand screening procedures, to screen for (ant)agonists, and in diagnostic assays. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)

RESULT 2  
 AAR99690  
 ID AAR99690 standard; protein; 1106 AA.  
 XX AAR99690;  
 AC AAR99690;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 11-OCT-1996 (first entry)  
 XX  
 DE Platelet-derived growth factor receptor.  
 XX  
 KW Platelet-derived growth factor receptor; PDGF-R; peptide dimer;  
 KW protein secretion; agonist; antagonist.  
 XX  
 OS Homo sapiens.  
 XX  
 XX EP721983-A1.  
 XX  
 PD 17-JUL-1996.  
 PF 18-JAN-1989; 95EP-00118567.  
 PR 22-JAN-1988; 88US-00146877.  
 PR 18-JAN-1989; 89EP-00100787.  
 XX  
 PA (ZYMO) ZYMOGENETICS INC.  
 XX  
 XX Sledziewski AZ, Bell LA, Kindsvogel WR;  
 DR WPI; 1996-322833/33.  
 DR N-PSDB; AAT34552.

Db 121 PDPTVGLPNDABELFIFLITEITIPCRVTDQQLVVTLHEKKGDAVALPVPVDHQRGFS 180  
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240  
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240  
QY 241 DVNFWNTYPRKESGRLEVPVTDFFLDMPYHRSILHIPSABELEDSTGTYTCNVTSVNDH 300  
Db 241 EVNFWNTYPRKESGRLEVPVTDFFLDMPYHRSILHIPSABELEDSTGTYTCNVTSVNDH 300  
QY 301 QDEKAINITVSGYVRLGEGVTLOFAELHRSRTLOVVFAYPPPTVLWFKDNRTLGD 360  
Db 301 QDEKAINITVSGYVRLGEGVTLOFAELHRSRTLOVVFAYPPPTVLWFKDNRTLGD 360  
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQLOQINVPVRL 420  
Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEOVLSFQLOQINVPVRL 420  
QY 421 ELSHSDPDGEGQVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480  
Db 421 ELSHSDPDGEGQVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETNV 480  
QY 481 TYWEEEOEFVWSTLRQVDRPLSVRCTLRNAVGODTOEVIIVPHSLPKVVIISAIIA 540  
Db 481 TYWEEEOEFVWSTLRQVDRPLSVRCTLRNAVGODTOEVIIVPHSLPKVVIISAIIA 540  
QY 541 LVVLTTISLIILMLQKKPRYRIRKWKVIESVSSDGHVYIYDPMQLPYDSTWELPRDQL 600  
Db 541 LVVLTTISLIILMLQKKPRYRIRKWKVIESVSSDGHVYIYDPMQLPYDSTWELPRDQL 600  
QY 601 VLGRITLGSAGFGQVVEATAGHLSHQATWKVAVKMLKSTARSEKQALMSELKIMSHLGP 660  
Db 601 VLGRITLGSAGFGQVVEATAGHLSHQATWKVAVKMLKSTARSEKQALMSELKIMSHLGP 660  
QY 661 HLNVNLLGACTGGGIYIITEICRYGDLVDYLHRNKHTFLQHSKRRPPSAELYSNAL 720  
Db 661 HLNVNLLGACTGGGIYIITEICRYGDLVDYLHRNKHTFLQHSKRRPPSAELYSNAL 720  
QY 721 PVGLPLPSVSLTGSDGGYMDMSKDESVDYVPMQDKGDKVYADIESNNYAPYDNYVP 780  
Db 721 PVGLPLPSVSLTGSDGGYMDMSKDESVDYVPMQDKGDKVYADIESNNYAPYDNYVP 780  
QY 781 SAPERTCRATLINESPVLSDMLVGFYSQVANGMEFLASKNCVHRDLAARNVLICSGKLV 840  
Db 781 SAPERTCRATLINESPVLSDMLVGFYSQVANGMEFLASKNCVHRDLAARNVLICSGKLV 840  
QY 841 KICDFGLARDIMRDSNYISKGSTFLPKWAPESIFNSLYTTLSDYVMSFGILLWEIFTLG 900  
Db 841 KICDFGLARDIMRDSNYISKGSTFLPKWAPESIFNSLYTTLSDYVMSFGILLWEIFTLG 900  
QY 901 GTPYPPLPNEQFYNAIKRGYMAQPAHASDEIYEMQKWEKFEIRPPFSQVLVLLER 960  
Db 901 GTPYPPLPNEQFYNAIKRGYMAQPAHASDEIYEMQKWEKFEIRPPFSQVLVLLER 960  
QY 961 LLGEGYKKYQVDEEFLRSDHAILRSQARLPFGHGLRSPDTSVLYTAQVQNEGDND 1020  
Db 961 LLGEGYKKYQVDEEFLRSDHAILRSQARLPFGHGLRSPDTSVLYTAQVQNEGDND 1020  
QY 1021 YIIPLDPKPEVADGEPGLSGSLASTNEVNTSTISCDSPLQDEPEPEPQLEQV 1080  
Db 1021 YIIPLDPKPEVADGEPGLSGSLASTNEVNTSTISCDSPLQDEPEPEPQLEQV 1080  
QY 1081 EPEPELEQLPDSCGCPAPRAEADSFL 1106  
Db 1081 EPEPELEQLPDSCGCPAPRAEADSFL 1106

RESULT 3  
ID ABP96311  
XX standard; protein; 1106 AA.  
AC ABP96311;  
XX

DT 20-MAY-2003 (first entry)  
XX Human platelet-derived growth factor receptor beta protein.  
DE Humanised baculovirus; cytotstatic; gene therapy; baculovirus; cancer;  
XX prostate cancer; platelet-derived growth factor receptor beta;  
KW chromosome 5.  
KW Homo sapiens.  
OS WO2003016540-A2.  
XX 27-FEB-2003.  
XX 15-AUG-2002; 2002WO-GB003791.  
XX 15-AUG-2001; 2001GB-00019852.  
XX (UYYO-) UNIV YORK.  
PA Maitland N;  
XX WPI; 2003-268336/26.  
XX New baculovirus having a modified genome encoding a therapeutic agent,  
PT useful in the manufacture of a medicament for the treatment of cancer,  
PT particularly prostate cancer.  
XX Claim 33; Page; 34pp; English.  
XX The present invention describes a humanised baculovirus (I) which  
CC comprises a modified baculovirus genome having a nucleic acid molecule  
CC encoding a therapeutic agent and a polypeptide which functions to target  
CC the baculovirus to at least one cell type. Also described is a  
CC pharmaceutical composition comprising (I). (I) has cytostatic activity,  
CC and can be used in gene therapy. The baculovirus is useful in the  
CC manufacture of a medicament for the treatment of cancer, particularly  
CC prostate cancer. The present sequence represents the human platelet-  
CC derived growth factor receptor beta protein, which is specified in the  
CC exemplification of the present invention. N.B. The present sequence is  
CC not given in the specification but is referred to in Claim 33 as Genbank  
CC accession number NM\_002609  
SQ Sequence 1106 AA;

Query Match 99.9%; Score 5762; DB 6; Length 1106;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRLPGAMPALALKGELLALLSLLLEPQISQGLVVTTPPGPELVNVSTFVLTCGSAVP 60  
Db 1 MRLPGAMPALALKGELLALLSLLLEPQISQGLVVTTPPGPELVNVSTFVLTCGSAVP 60  
QY 61 VVERMSQEPPOEMAQAQDGTFSVLTNLTLGLDTGEYFCTHNDRSGLETDERKRLYIFV 120  
Db 61 VVERMSQEPPOEMAQAQDGTFSVLTNLTLGLDTGEYFCTHNDRSGLETDERKRLYIFV 120  
QY 121 PDPTVGLPNDABELFIFLITEITIPCRVTDQQLVVTLHEKKGDAVALPVPVDHQRGFS 180  
Db 121 PDPTVGLPNDABELFIFLITEITIPCRVTDQQLVVTLHEKKGDAVALPVPVDHQRGFS 180  
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240  
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240  
QY 241 DVNFWNTYPRKESGRLEVPVTDFFLDMPYHRSILHIPSABELEDSTGTYTCNVTSVNDH 300  
Db 241 EVNFWNTYPRKESGRLEVPVTDFFLDMPYHRSILHIPSABELEDSTGTYTCNVTSVNDH 300  
QY 301 QDEKAINITVSGYVRLGEGVTLOFAELHRSRTLOVVFAYPPPTVLWFKDNRTLGD 360  
Db 301 QDEKAINITVSGYVRLGEGVTLOFAELHRSRTLOVVFAYPPPTVLWFKDNRTLGD 360

QY 361 SAGEIATLSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSPQLQINVPVRVL 420  
DB 361 SAGEIATLSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSPQLQINVPVRVL 420  
QY 421 ELSSEHPDSEGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSESEESQLETVN 480  
DB 421 ELSSEHPDSEGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSESEESQLETVN 480  
QY 481 TYWEEEOEFVNSTLRLOHVDRLPVRCTLRNAVGDQTOEVIWVPHSLPKVWVISAAILA 540  
DB 481 TYWEEEOEFVNSTLRLOHVDRLPVRCTLRNAVGDQTOEVIWVPHSLPKVWVISAAILA 540  
QY 541 LVVLTIIISIIILMLWKKPRYIEIRKWKVIESVSSDGHYIYVDPMPOLPYDSTWELPRDQL 600  
DB 541 LVVLTIIISIIILMLWKKPRYIEIRKWKVIESVSSDGHYIYVDPMPOLPYDSTWELPRDQL 600  
QY 601 VLGRTLGSAGFQVVEATAGHLSHQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660  
DB 601 VLGRTLGSAGFQVVEATAGHLSHQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660  
QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDVYLHRNKHTFLOHHSDDKRRPPSAELYSNAL 720  
DB 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDVYLHRNKHTFLOHHSDDKRRPPSAELYSNAL 720  
QY 721 PVGLPLPSHVSLTGSDGGYMDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAPYDNYVP 780  
DB 721 PVGLPLPSHVSLTGSDGGYMDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAPYDNYVP 780  
QY 781 SAPERTCRATLINESPVLGYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLIICBGLV 840  
DB 781 SAPERTCRATLINESPVLGYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLIICBGLV 840  
QY 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
DB 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
QY 901 GTPYPLPWNQFYNAIKGYRMAQPAHASDEIYIMQKWEKFEIRPFQVLLVLLER 960  
DB 901 GTPYPLPWNQFYNAIKGYRMAQPAHASDEIYIMQKWEKFEIRPFQVLLVLLER 960  
QY 961 LLGEGYKKYQQVDEEFLRSDHPAILRQARLPGFHGLRSPDLDTSSVLYTAVQPNEGDND 1020  
DB 961 LLGEGYKKYQQVDEEFLRSDHPAILRQARLPGFHGLRSPDLDTSSVLYTAVQPNEGDND 1020  
QY 1021 YIIPDPKPVEADEGLSGSPSLASSTINEVNTSTISCDSPLQDEPEPEPQLELOV 1080  
DB 1021 YIIPDPKPVEADEGLSGSPSLASSTINEVNTSTISCDSPLQDEPEPEPQLELOV 1080  
QY 1081 EPEPELEQLPDGCPAPRAEADSFL 1106  
DB 1081 EPEPELEQLPDGCPAPRAEADSFL 1106

RESULT 4  
ID ABR84719  
XX ABR84719 standard; protein; 1106 AA.  
AC ABR84719;  
XX 18-DEC-2003 (first entry)  
DT Human PDGF beta receptor protein.  
DE Tissue vascularisation; aging; mouse; human; PDGF A; PDGF B;  
KW PDGF alpha receptor; PDGF beta receptor; endothelial precursor cell;  
KW vascular disease; cardiant; cell therapy.  
XX Homo sapiens.  
OS  
XX WO2003070083-A2.  
PN  
XX 28-AUG-2003.  
PD  
XX

PF 13-FEB-2003; 2003WO-US004244.  
XX  
PR 15-FEB-2002; 2002US-0357328P.  
PR 08-AUG-2002; 2002WO-US025175.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
PA (EDEL/) EDELBERG J M.  
PA (RAFI/) RAFII S.  
PA (HONG/) HONG M K.  
PA (LANZ/) LANZA R P.  
PA (WEST/) WEST M D.  
XX  
PI Edelberg JM, Rafii S, Hong MK, Lanza RP, West MD;  
XX WPI; 2003-697548/66.  
XX  
PT Treating a vascular condition, e.g. myocardial infarction,  
PT atherosclerosis, ischemia, congestive heart failure, hypertension,  
PT stroke, thrombosis, arrhythmia or tachycardia, by administering  
PT endothelial precursor cells.  
XX  
PS Claim 24; Page 47-48; 110pp; English.  
XX  
CC The present invention relates to a method of treating a vascular  
CC condition in a mammal, which comprises administering to the mammal a  
CC therapeutic amount of endothelial precursor cells. The method and cells  
CC of the invention are useful for treating a vascular condition, e.g.  
CC myocardial infarction, atherosclerosis, ischemia, tachycardia,  
CC congestive heart failure, peripheral vasculature disorder, hypertension,  
CC stroke, thrombosis, arrhythmia or tachycardia. The present sequence is a  
CC protein shown in the exemplification of the invention  
XX  
SQ Sequence 1106 AA;  
Query Match 99.9%; Score 5762; DB 7; Length 1106;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRLPGAMPALAKGELLISLLSLLLEPOISQGLVWTPPGPELVNVSFVLTCSGSAPV 60  
DB 1 MRLPGAMPALAKGELLISLLSLLLEPOISQGLVWTPPGPELVNVSFVLTCSGSAPV 60  
QY 61 VWRMSQEPPEQWAKAQDGTFSVLTNLTLGLDTGEYFCTHNSRGLTDERKRLYIFV 120  
DB 61 VWRMSQEPPEQWAKAQDGTFSVLTNLTLGLDTGEYFCTHNSRGLTDERKRLYIFV 120  
QY 121 PDPTVGLFNDABELFIFLITEITPCRVTDPPQLVTLHEKKGVALPVPYDHORGFS 180  
DB 121 PDPTVGLFNDABELFIFLITEITPCRVTDPPQLVTLHEKKGVALPVPYDHORGFS 180  
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240  
DB 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN 240  
QY 241 DVNFWNTYPRKESGRVLEPVTDFLLDMPYHRSILHIPSABLEDSTYTCNVTSVNDH 300  
DB 241 EVNFWNTYPRKESGRVLEPVTDFLLDMPYHRSILHIPSABLEDSTYTCNVTSVNDH 300  
QY 301 ODEKAINITVSEGVYRLGEGVTGLOFAELHRSRTLOVVFEPPTVLWEKDNRTLGD 360  
DB 301 ODEKAINITVSEGVYRLGEGVTGLOFAELHRSRTLOVVFEPPTVLWEKDNRTLGD 360  
QY 361 SAGEIATLSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSPQLQINVPVRVL 420  
DB 361 SAGEIATLSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSPQLQINVPVRVL 420  
QY 421 ELSSEHPDSEGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSESEESQLETVN 480  
DB 421 ELSSEHPDSEGEQTVRCRGRMPQPNIIWSACRDLKRCPRELPTLLGNSESEESQLETVN 480  
QY 481 TYWEEEOEFVNSTLRLOHVDRLPVRCTLRNAVGDQTOEVIWVPHSLPKVWVISAAILA 540  
DB 481 TYWEEEOEFVNSTLRLOHVDRLPVRCTLRNAVGDQTOEVIWVPHSLPKVWVISAAILA 540

QY 541 LVVLTIIISLIILMLWQKPRYIRWKVIESVSSDGEHYIYVDPMLPYDSTWELPRDQL 600  
 DB 541 LVVLTIIISLIILMLWQKPRYIRWKVIESVSSDGEHYIYVDPMLPYDSTWELPRDQL 600  
 QY 601 VLGRITLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660  
 DB 601 VLGRITLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660  
 QY 661 HLNVNLLGACTKGGPIIYITEYCRYGDLVDYLHRNKHTFLOHSDKRPPSPSAELYSNAL 720  
 DB 661 HLNVNLLGACTKGGPIIYITEYCRYGDLVDYLHRNKHTFLOHSDKRPPSPSAELYSNAL 720  
 QY 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMKMGDKVYADIESNNAPYDNYVP 780  
 DB 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMKMGDKVYADIESNNAPYDNYVP 780  
 QY 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICGKLV 840  
 DB 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICGKLV 840  
 QY 841 KICDFGLARDIMRDSNYISKGSTFPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
 DB 841 KICDFGLARDIMRDSNYISKGSTFPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
 QY 901 GTPYPELPWNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQLVLLER 960  
 DB 901 GTPYPELPWNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQLVLLER 960  
 QY 961 LLGEGYKKYQQVDEBFLRSDHPAILRSQARLPFGHLSPLDTSVLYTAVQPNEGDND 1020  
 DB 961 LLGEGYKKYQQVDEBFLRSDHPAILRSQARLPFGHLSPLDTSVLYTAVQPNEGDND 1020  
 QY 1021 YIIPLPDPKPEVADEGLSGSPSLASTINEVNTSTISCDSPLEPQDEPEPEPQLELQV 1080  
 DB 1021 YIIPLPDPKPEVADEGLSGSPSLASTINEVNTSTISCDSPLEPQDEPEPEPQLELQV 1080  
 QY 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106  
 DB 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106  
 RESULT 5  
 ADF45082  
 ID ADF45082 standard; protein; 1106 AA.  
 AC ADF45082;  
 XX ADF45082;  
 DT 12-FEB-2004 (first entry)  
 DE Human kinase PDGFR-b.  
 KW Human; protein kinase; enzyme; inhibitor; PDGFR-b.  
 XX Homo sapiens.  
 OS WO2003081210-A2.  
 PN 02-OCT-2003.  
 XX 20-MAR-2003; 2003WO-US008725.  
 PR 21-MAR-2002; 2002US-0366892P.  
 XX (SUNE-) SUNESIS PHARM INC.  
 PA Prescott JC, Braisted A;  
 XX WPI; 2003-865136/80.  
 PT Identifying ligand binding to inactive conformation of target protein  
 PT kinase (T) comprises contacting the conformation modified (T) which  
 PT contains reactive group at binding site, with ligands and detecting

kinase-ligand conjugate formation.  
 Disclosure; SEQ ID NO 51; 260pp; English.  
 CC The present invention relates to a method for identifying a ligand (L),  
 CC which binds to an inactive conformation of target protein kinase (T). The  
 CC method involves contacting inactive conformation of (T), which contains  
 CC or is modified to contain a reactive group at or near a binding site of  
 CC interest, with one or more ligand candidates capable of covalently  
 CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).  
 CC The method is useful for identifying protein kinase inhibitors that  
 CC preferentially bind to inactive conformation of a target protein kinase.  
 CC The present sequence is a protein kinase which may be modified via an  
 CC amino acid substitution, for use in the method of the invention.  
 XX Sequence 1106 AA;  
 SQ  
 Query Match 99.9%; Score 5762; DB 7; Length 1106;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRLPGAMPALALKGELLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSSAPV 60  
 DB 1 MRLPGAMPALALKGELLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSSAPV 60  
 QY 61 VMERMSQEPPEMAKAQDGTFFSVLTTLNLTLGLDTGEYFCTHNDRGLTDERKRLYIFV 120  
 DB 61 VMERMSQEPPEMAKAQDGTFFSVLTTLNLTLGLDTGEYFCTHNDRGLTDERKRLYIFV 120  
 QY 121 PPTVGLFENDABELFIFLITEITIPCRVTDLPQLVTLHEKKGDVALPVVDHORGFS 180  
 DB 121 PPTVGLFENDABELFIFLITEITIPCRVTDLPQLVTLHEKKGDVALPVVDHORGFS 180  
 QY 181 GFEDRSYICKTTIGDREVDSDAYVYRLOVSSINVSNAVQTVVRQGENITLMCVIGN 240  
 DB 181 GFEDRSYICKTTIGDREVDSDAYVYRLOVSSINVSNAVQTVVRQGENITLMCVIGN 240  
 QY 241 DVNFENTWYPRKESGRLEVPVTDFFLLDMPYHRSILHIPSAAELSDSGTTCNVTESVNDH 300  
 DB 241 EVNFENTWYPRKESGRLEVPVTDFFLLDMPYHRSILHIPSAAELSDSGTTCNVTESVNDH 300  
 QY 301 QDEKAINITVWESGYVRLLEGEVGTQFAELHRSRTLOVFEAYPPPTVLFWKDNRITLGD 360  
 DB 301 QDEKAINITVWESGYVRLLEGEVGTQFAELHRSRTLOVFEAYPPPTVLFWKDNRITLGD 360  
 QY 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTWRAFEDAEVQLSFQQLINVPVRVL 420  
 DB 361 SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTWRAFEDAEVQLSFQQLINVPVRVL 420  
 QY 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480  
 DB 421 ELSSEHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETNV 480  
 QY 481 TYWEEBQEFVYSTLRQLQVDRPLSVRCITLRNAVQDQTEVIVVPHSLPFKVVIVSAILA 540  
 DB 481 TYWEEBQEFVYSTLRQLQVDRPLSVRCITLRNAVQDQTEVIVVPHSLPFKVVIVSAILA 540  
 QY 541 LVVLTIIISLIILMLWQKPRYIRWKVIESVSSDGEHYIYVDPMLPYDSTWELPRDQL 600  
 DB 541 LVVLTIIISLIILMLWQKPRYIRWKVIESVSSDGEHYIYVDPMLPYDSTWELPRDQL 600  
 QY 601 VLGRITLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660  
 DB 601 VLGRITLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660  
 QY 661 HLNVNLLGACTKGGPIIYITEYCRYGDLVDYLHRNKHTFLOHSDKRPPSPSAELYSNAL 720  
 DB 661 HLNVNLLGACTKGGPIIYITEYCRYGDLVDYLHRNKHTFLOHSDKRPPSPSAELYSNAL 720  
 QY 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMKMGDKVYADIESNNAPYDNYVP 780  
 DB 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMKMGDKVYADIESNNAPYDNYVP 780

QY 781 SAPERTCRATLINESPVLSDYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICGKLV 840  
 Db |||||  
 QY 841 KICDFGLARDIMRDSNYISKGSFTFLPKWMAPEISFNLSYTTLSDVMSFGILLWEFTLG 900  
 Db |||||  
 QY 901 GTPYPELPWNEOFYNAIKGGRMAQPAHASDEIYELWQKWEKFEIRPPFSOLVLLER 960  
 Db |||||  
 QY 961 LLGEGYKKYQVDEBFLRSDHPAILRSQARLPFGHLSPLDTSVLYTAVQPNEGDND 1020  
 Db |||||  
 QY 1021 YIIPDPKPVEADEGPLEGSPSLASTNLNEVNTSITSCDSPLEPQDBPEPPELQV 1080  
 Db |||||  
 QY 1081 EPEPELEQLPDSGCPAPRAEADSFL 1106  
 Db |||||  
 RESULT 6  
 ID ABO84679 standard; protein; 1106 AA.  
 AC ABO84679;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human cancer-associated protein HP20-018.3.  
 XX  
 KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;  
 KW Lymphoma; CAP.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004074320-A2.  
 XX  
 PD 02-SEP-2004.  
 XX  
 PF 17-FEB-2004; 2004WO-US0004730.  
 XX  
 PR 14-FEB-2003; 2003US-00367094.  
 PR 15-MAR-2003; 2003US-00388838.  
 PR 15-APR-2003; 2003US-00417375.  
 PR 13-JUN-2003; 2003US-00461862.  
 PR 15-SEP-2003; 2003US-00663431.  
 PR 15-DEC-2003; 2003US-00737318.  
 XX  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 XX  
 PI Morris DW, Morris DW, Malandro MG;  
 DR  
 DR WPI: 2004-652914/63.  
 DR N-PSDB; ABO32965.  
 XX  
 FT New isolated cancer-associated polynucleotides and polypeptides useful  
 PT for diagnosing, preventing or treating cancers, especially lymphoma and  
 PT leukemia, or in screening for agents that modulate cancer.  
 XX  
 PS claim 18; seqid 710; 310pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising at least 10  
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given  
 CC in the specification, or its complement. The nucleic acids encode cancer-  
 CC associated proteins. Also included are an expression vector comprising  
 CC the isolated nucleic acid cited above, a host cell comprising the above  
 CC recombinant nucleic acid or expression vector, a microarray for detecting  
 CC a cancer-associated (CA) nucleic acid comprising at least one probe

CC comprising at least 10 contiguous nucleotides of any of the above-  
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within  
 CC an open reading frame of a CA sequence selected from any of the 95  
 CC polynucleotide sequences as mentioned in the specification, or its  
 CC complement), an isolated antibody, (or its antigen binding fragment) that  
 CC binds to the above polypeptide, a hybridoma that produces the above  
 CC monoclonal antibody, a pharmaceutical composition comprising the above  
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer  
 CC cells (comprising the antibody cited above, methods for diagnosing cancer  
 CC or for detecting the presence or absence of cancer cells in an  
 CC individual, a method for inhibiting growth of cancer cells in an  
 CC individual, a method for delivering a therapeutic agent to cancer cells  
 CC in an individual, an electronic library comprising the above  
 CC polynucleotide or polypeptide (or their fragments), methods of screening  
 CC for anticancer activity or for a bioactive agent capable of modulating  
 CC the activity of a CA protein (CAP), methods for detecting cancer  
 CC associated with expression of a polypeptide in a test cell sample, a  
 CC method for treating cancers and a method for inhibiting the expression of  
 CC CA gene in a cell. The composition and methods are useful for detecting,  
 CC diagnosing, preventing and treating cancers, especially lymphoma and  
 CC leukaemia. These may also be used in screening for agents that modulate  
 CC cancer. The present sequence is a human CAP protein sequence. NOTE: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1106 AA;  
 Query Match 99.9%; Score 5762; DB 8; Length 1106;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRLPGAMPALALKGELLLSLLLELPQISQGLVVTTPGPELVNVSSFTVLTCSGAPV 60  
 Db |||||  
 QY 1 MRLPGAMPALALKGELLLSLLLELPQISQGLVVTTPGPELVNVSSFTVLTCSGAPV 60  
 Db |||||  
 QY 61 VWERMSQEPPOEMAKAQDGTFFSVLTLTNLTLGLDTGEYFCTHNSRGLTDERKRLYIFV 120  
 Db |||||  
 QY 61 VWERMSQEPPOEMAKAQDGTFFSVLTLTNLTLGLDTGEYFCTHNSRGLTDERKRLYIFV 120  
 Db |||||  
 QY 121 PDPTVGFLNDABELFIFLITEITPCRVTDLPQVLTHEKKGDAVALPYVDHORGFS 180  
 Db |||||  
 QY 121 PDPTVGFLNDABELFIFLITEITPCRVTDLPQVLTHEKKGDAVALPYVDHORGFS 180  
 Db |||||  
 QY 181 GIFEDRSYICKTIGDREVDSDAYVYRQVSSINVSNVAVQTVRQGENITLMCIIGN 240  
 Db |||||  
 QY 181 GIFEDRSYICKTIGDREVDSDAYVYRQVSSINVSNVAVQTVRQGENITLMCIIGN 240  
 Db |||||  
 QY 241 DVVNFETVYPRKESGRLVEPVTDFLLDMPYHRSILHIPSABLESDSGTYTCNVTSVNDH 300  
 Db |||||  
 QY 241 EVVNFETVYPRKESGRLVEPVTDFLLDMPYHRSILHIPSABLESDSGTYTCNVTSVNDH 300  
 Db |||||  
 QY 301 QDEKAINITVSGYVRLIGEVGTLQFAELHSRSLTQVVFAYPPPTVLMFKDNRTLGD 360  
 Db |||||  
 QY 301 QDEKAINITVSGYVRLIGEVGTLQFAELHSRSLTQVVFAYPPPTVLMFKDNRTLGD 360  
 Db |||||  
 QY 361 SAGETALSTRNVSETRYVSELTILVRKVAAEAGHYTRAFHEDAEOVLSQQLQINVPVRL 420  
 Db |||||  
 QY 361 SAGETALSTRNVSETRYVSELTILVRKVAAEAGHYTRAFHEDAEOVLSQQLQINVPVRL 420  
 Db |||||  
 QY 421 ELSSEHPDSGEQTVRCRGMPQPNIIWSACRDLKRCPRELPPTLLGNSESEESQLETVN 480  
 Db |||||  
 QY 421 ELSSEHPDSGEQTVRCRGMPQPNIIWSACRDLKRCPRELPPTLLGNSESEESQLETVN 480  
 Db |||||  
 QY 481 TYWESEOEPEVYSTLRLOHVDRLPSVRCCTLRNAVGDQTOEVIWVPHSLPFKVVVISAIIA 540  
 Db |||||  
 QY 481 TYWESEOEPEVYSTLRLOHVDRLPSVRCCTLRNAVGDQTOEVIWVPHSLPFKVVVISAIIA 540  
 Db |||||  
 QY 541 LVVLVTIISIIILMLWQKKPRYEIRKWKVIESVSSDGEHYIYVDPMLQPYDSTWELPRDQL 600  
 Db |||||  
 QY 541 LVVLVTIISIIILMLWQKKPRYEIRKWKVIESVSSDGEHYIYVDPMLQPYDSTWELPRDQL 600  
 Db |||||  
 QY 601 VLGRITLGSAGFCQVVEATAHGLSHSQATMKVAVKMLKSTARSEKQALMSELKIMSHLGP 660  
 Db |||||

Db 601 VLGRITLGSAGFCQVWEATAGHLSHQATMKVAVQMLKSTARSEKQALMSELKIMSHLGP 660  
Qy 661 HLNVNLLGACTKGGPIYIITEYCRGYDLVDYLHRNKHTFLOHSHDKRPPSAELYSNAL 720  
Db 661 HLNVNLLGACTKGGPIYIITEYCRGYDLVDYLHRNKHTFLOHSHDKRPPSAELYSNAL 720  
Qy 721 PVGLPLPSHVSLSGESGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780  
Db 721 PVGLPLPSHVSLSGESGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP 780  
Qy 781 SAPERTCRATLINESVLSYMDLVGRSYQVANGMEFLASNCVHRDLAARNVLIICEGKLV 840  
Db 781 SAPERTCRATLINESVLSYMDLVGRSYQVANGMEFLASNCVHRDLAARNVLIICEGKLV 840  
Qy 841 KICDFGLARDIMRDSNYISKGSTFPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
Db 841 KICDFGLARDIMRDSNYISKGSTFPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
Qy 901 GTPYPELPNEQFYNAIKRGYMAQPAHASDEIYEIMQKCWEKFEIRPPFSQVLVLLER 960  
Db 901 GTPYPELPNEQFYNAIKRGYMAQPAHASDEIYEIMQKCWEKFEIRPPFSQVLVLLER 960  
Qy 961 LLGEGYKKYQVDEEFLRSDHPAILRSQARLPGFHGLRSPDTSVLTVAVQPNEGDND 1020  
Db 961 LLGEGYKKYQVDEEFLRSDHPAILRSQARLPGFHGLRSPDTSVLTVAVQPNEGDND 1020  
Qy 1021 YIIPLPDPKPEVADEGLSGSLASSTINEVNTSITSCDSPLEPQDEPEPEPQLELOV 1080  
Db 1021 YIIPLPDPKPEVADEGLSGSLASSTINEVNTSITSCDSPLEPQDEPEPEPQLELOV 1080  
Qy 1081 EPEPELEQLPDGSCAPRAEADSFL 1106  
Db 1081 EPEPELEQLPDGSCAPRAEADSFL 1106  
RESULT 7  
ABG72459  
ID ABG72459 standard; protein; 1106 AA.  
AC ABG72459;  
XX  
XX  
XX 13-FEB-2003 (first entry)  
XX  
XX Human platelet derived growth factor receptor beta mutant L867M.  
DE  
DE Human; platelet derived growth factor receptor beta; PDGFRbeta;  
KW hepatotropic; dermatological; nephrotropic; vulnerable; ophthalmological;  
KW cytostatic; gene therapy; vaccine; phosphoinositide-kinase-inhibitor-3;  
KW phospholipase-inhibitor-C; receptor tyrosine kinase; cell proliferation;  
KW cell migration; extracellular matrix synthesis; secretion;  
KW liver contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;  
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;  
KW mutant; mutein.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..32  
FT /label= Signal\_peptide  
FT Protein 33..1106  
FT /label= Mature\_PDGRF\_beta  
FT Domain 227..298  
FT /label= Immunoglobulin-like\_domain  
FT Domain 335..398  
FT /label= Immunoglobulin-like\_domain  
FT Domain 532..556  
FT /label= Transmembrane\_domain  
FT Domain 604..694  
FT /notes "Split tyrosine kinase domain segment 1"  
FT 799..951

FT Misc-difference 867 /note= "Split tyrosine kinase domain segment 2"  
FT /note= "Wild type Leu substituted by Met"  
XX  
PN US2002111304-A1.  
XX  
PD 15-AUG-2002.  
XX  
XX 25-MAY-2001; 2001US-00866510.  
XX  
XX 01-DEC-2000; 2000US-0250747P.  
PR 07-MAY-2001; 2001US-0289103P.  
XX  
XX (KAZL/) KAZLAUSKAS A.  
PA (IKUN/) IKUNO Y.  
XX  
XX Kazlauskas A, Ikuno Y;  
XX WPI; 2003-066697/06.  
DR N-PSDB; ABS57790.  
XX  
XX New polypeptide for treating or preventing diseases associated with an  
PT abnormal platelet-derived growth factor (PDGF) level; e.g. cell  
PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha  
PT or -beta.  
XX  
XX Claim 7; Page 101-104; 127pp; English.  
PS  
XX  
XX The invention describes a polypeptide comprising a portion of the  
CC receptor tyrosine kinase platelet-derived growth factor alpha receptor  
CC (PDGFalpha). The polypeptide and the polynucleotide are useful in  
CC treating or preventing diseases and conditions associated with an  
CC abnormal PDGF level or response, such as cell proliferation, cell  
CC migration, extracellular matrix synthesis and secretion or cell  
CC contraction. Exemplary diseases or disorders include cell proliferative  
CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g. fibrosis,  
CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,  
CC scleroderma, keloids, hypertrophic scars, skin wound healing or  
CC proliferative vitreoretinopathy). The method may be used in identifying  
CC compounds for treating or preventing the development of diseases  
CC involving cell contraction, e.g. fibrotic diseases. This is the amino  
CC acid sequence of human platelet derived growth factor receptor (PDGFR)  
XX beta mutant L867M  
XX  
SQ Sequence 1106 AA;  
Query Match 99.9%; Score 5760; DB 6; Length 1106;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1104; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRLPGMPALALKGELLLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCGSAVP 60  
Db 1 MRLPGMPALALKGELLLSLLLEPQISQGLVVTTPGPELVNVSSTFVLTCGSAVP 60  
Qy 61 VMERMSQPPQEMAKAQDGTFSVLTNLNLTGLDTGEVFTCHNDSRGLTDERKRLYIFV 120  
Db 61 VMERMSQPPQEMAKAQDGTFSVLTNLNLTGLDTGEVFTCHNDSRGLTDERKRLYIFV 120  
Qy 121 PDPTVGFPLNDAAELFIPLTEITETIPCRVTDPOLVTLHEKKGDAVALPVPYDHRGFS 180  
Db 121 PDPTVGFPLNDAAELFIPLTEITETIPCRVTDPOLVTLHEKKGDAVALPVPYDHRGFS 180  
Qy 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240  
Db 181 GIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCVIGN 240  
Qy 241 DVVNFETWYPRKESGRLVEPVTDFLLDMPYHRSILHIPSABELEDGTYTCNVTSVNDH 300  
Db 241 EVVNFETWYPRKESGRLVEPVTDFLLDMPYHRSILHIPSABELEDGTYTCNVTSVNDH 300  
Qy 301 QDEKAINITVWESGYVRLGEGVTGLQFAELHRSRTLOVFEAYPPPTVLMFKDNRITLGD 360  
Db 301 QDEKAINITVWESGYVRLGEGVTGLQFAELHRSRTLOVFEAYPPPTVLMFKDNRITLGD 360

QY 361 SAGEIATLSTNVSSETRVSELTIVRVKVAEGHYTMRAFHEDEAEVQLSFQLOINVPVRVL 420  
DB |||||  
DB 361 SAGEIATLSTNVSSETRVSELTIVRVKVAEGHYTMRAFHEDEAEVQLSFQLOINVPVRVL 420  
QY 421 ELSSEHPDSGEQTVRCGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480  
DB |||||  
DB 421 ELSSEHPDSGEQTVRCGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480  
QY 481 TYWEEBQEFVSTLRLQVDRPLSVRCCTLRNAVQDQTOEVIIVPHSLPDKVVISAILA 540  
DB |||||  
DB 481 TYWEEBQEFVSTLRLQVDRPLSVRCCTLRNAVQDQTOEVIIVPHSLPDKVVISAILA 540  
QY 541 LVVLATISLIIILMLWQKPRYIEIRKWKVIESVSSDGHYIYVDPMLPYDSTWELPRDOL 600  
DB |||||  
DB 541 LVVLATISLIIILMLWQKPRYIEIRKWKVIESVSSDGHYIYVDPMLPYDSTWELPRDOL 600  
QY 601 VLGRITLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660  
DB |||||  
DB 601 VLGRITLGSAGFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660  
QY 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720  
DB |||||  
DB 661 HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPPSAELYSNAL 720  
QY 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMLDMKGVYADIESSNYMAPYDNYVP 780  
DB |||||  
DB 721 PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMLDMKGVYADIESSNYMAPYDNYVP 780  
QY 781 SAPERTCRATLINESPVLSDMLVGFSPYQVANGMEFLASKNCVHRDLAARNVLCIEGKLV 840  
DB |||||  
DB 781 SAPERTCRATLINESPVLSDMLVGFSPYQVANGMEFLASKNCVHRDLAARNVLCIEGKLV 840  
QY 841 KICDFGLARDIMRDSNYISKGSTFLPKWMAPEISFNSLYTTLSDVMSFGILLWEIFTLG 900  
DB |||||  
DB 841 KICDFGLARDIMRDSNYISKGSTFLPKWMAPEISFNSLYTTLSDVMSFGILLWEIFTLG 900  
QY 901 GTYPYPLPNEQFYNAIKRGYMAQPAHASDEIYEIMQKWEKEFIRPPFQSVLLLER 960  
DB |||||  
DB 901 GTYPYPLPNEQFYNAIKRGYMAQPAHASDEIYEIMQKWEKEFIRPPFQSVLLLER 960  
QY 961 LLGEGYKKYQVDEFFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020  
DB |||||  
DB 961 LLGEGYKKYQVDEFFLRSDHPAILRSQARLPGFHGLRSPDLTSSVLYTAVQPNEGDND 1020  
QY 1021 YIIPLPDPKPEVADEGLSGSPSLASSTINEVNTSTISCDSPLQDPEPEPEQLEQV 1080  
DB |||||  
DB 1021 YIIPLPDPKPEVADEGLSGSPSLASSTINEVNTSTISCDSPLQDPEPEPEQLEQV 1080  
QY 1081 EPEPELEQLPDGCPAPRAEADSFL 1106  
DB |||||  
DB 1081 EPEPELEQLPDGCPAPRAEADSFL 1106

RESULT 8  
AAR26205  
ID AAR26205 standard; protein; 1106 AA.  
XX AC AAR26205;  
XX DT 25-MAR-2003 (revised)  
XX DT 09-FEB-1993 (first entry)  
DE Type B human platelet-derived growth factor receptor.  
XX PDGF; PDGF-R; mesenchyme; tyrosine kinase; ligand binding region.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..32  
XX FT /label= Signal\_peptide  
XX FT 24..1106  
XX FT Protein

/label= Mature\_PDGF-B  
W09213867-A1.  
20-AUG-1992.  
28-JAN-1992; 92WO-US0000730.  
31-JAN-1991; 91US-00650793.  
(CORT-) COR THERAPEUTICS INC.  
Escobedo JA, Williams LT, Wolf D, Tomlinson JE, Pretto LJ;  
Giese NA;  
WPI; 1992-299970/36.  
N-PSDB; AAQ27447.  
Platelet derived growth factor receptor (PDGF-R) poly:peptide(s) - useful  
as therapeutic and diagnostic agents e.g. for assaying PDGF activity in  
sample.  
Disclosure; Page 75; 109pp; English.

The sequence given is one allele of type B human platelet-derived growth  
factor (PDGF) receptor (PDGF-R). This receptor is typically found on  
cells of mesenchymal origin. It acts while in the form of two  
transmembrane glycoproteins, each of which is about 180 kb. This receptor  
has three major regions. The first is a transmembrane region, which spans  
the membrane once, separating the regions of the receptor exterior to the  
cell from those interior to the cell. The second region is an  
extracellular region which contains the domains which bind the PDGF. The  
third region is an intracellular region which possesses a tyrosine kinase  
activity. This tyrosine kinase domain is notable in having an insert of  
approx. 100 amino acids, as compared with most other receptor tyrosine  
kinase domains which are contiguous or have shorter insert sequences.  
Fragments of this sequence between 8 and 400 amino acids comprising one  
or more PDGF ligand binding region from the extracellular domain may be  
used to bind a PDGF ligand. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 1106 AA;  
Query Match 99.9%; Score 5759; DB 2; Length 1106;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MRLPGAMPALALKGELLISLLELLEPOISQGLVVTTPGPELVLVNVSFTVLTCSGAPV 60  
DB |||||  
DB 1 MRLPGAMPALALKGELLISLLELLEPOISQGLVVTTPGPELVLVNVSFTVLTCSGAPV 60  
QY 61 VVERMSQEPPOEMAKAQDGTFSVLTNLTLGLDTGEYFCTHNDRGLTDERKRLYIFV 120  
DB |||||  
DB 61 VVERMSQEPPOEMAKAQDGTFSVLTNLTLGLDTGEYFCTHNDRGLTDERKRLYIFV 120  
QY 121 PDPTVGFPLNDABELFIFLITEITPCRVTDLPQVLTLLHEKKGVALPVYDHORGFS 180  
DB |||||  
DB 121 PDPTVGFPLNDABELFIFLITEITPCRVTDLPQVLTLLHEKKGVALPVYDHORGFS 180  
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYRQVSSINVSNAVQTVVRQGNITLMCIIGN 240  
DB |||||  
DB 181 GIFEDRSYICKTTIGDREVDSDAYVYRQVSSINVSNAVQTVVRQGNITLMCIIGN 240  
QY 241 DVVNFEWTPRKESGRVLEPVTDFLLDMPYHRSILHIPSABLESSTGTYTCNVTSVNDH 300  
DB |||||  
DB 241 DVVNFEWTPRKESGRVLEPVTDFLLDMPYHRSILHIPSABLESSTGTYTCNVTSVNDH 300  
QY 301 QDEKAINITVSEGVYRLLGEVGTLOFAELHESRTLOVVFAYPPPTVLFWKDNRTLGDS 360  
DB |||||  
DB 301 QDEKAINITVSEGVYRLLGEVGTLOFAELHESRTLOVVFAYPPPTVLFWKDNRTLGDS 360  
QY 361 SAGEIATLSTNVSSETRVSELTIVRVKVAEGHYTMRAFHEDEAEVQLSFQLOINVPVRVL 420  
DB |||||  
DB 361 SAGEIATLSTNVSSETRVSELTIVRVKVAEGHYTMRAFHEDEAEVQLSFQLOINVPVRVL 420





Db 121 PDVTGFLPNDABELFLFTEITETPCRTVDPQLVVTLEKKGVALPVPDQHGRFS 180  
 Qy 181 GIFEDRSYIKTKTIGREVSDSDAYVYVRLQVSSINVSNAVQTVVRGENITLMCMVIGN 240  
 Db 181 GIFEDRSYIKTKTIGREVSDSDAYVYVRLQVSSINVSNAVQTVVRGENITLMCMVIGN 240  
 Qy 241 DVNFEWTPKESGRLEVPVTDPLDMPVHISILHIPSAAELEDGTYTCNVTVESVNDH 300  
 Db 241 DVNFEWTPKESGRLEVPVTDPLDMPVHISILHIPSAAELEDGTYTCNVTVESVNDH 300  
 Qy 301 QDEKAINITVSGYVRLLEGEVGTQFAELHRSRTLQVVFPEAYPPPTVLMFKDNRITLGD 360  
 Db 301 QDEKAINITVSGYVRLLEGEVGTQFAELHRSRTLQVVFPEAYPPPTVLMFKDNRITLGD 360  
 Qy 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTWRAFHEDAEOVLSFOLQINVPVRL 420  
 Db 361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTWRAFHEDAEOVLSFOLQINVPVRL 420  
 Qy 421 ELSHSPDSGEQTVRCGRGMPOPNIIWSACRDLKCPRELPTLLGNSEESOLETNV 480  
 Db 421 ELSHSPDSGEQTVRCGRGMPOPNIIWSACRDLKCPRELPTLLGNSEESOLETNV 480  
 Qy 481 TYWEEQEPEVWSTLRLQVDRPLSVRCRLRNAGVQDTQEVIVVPHSLPFPKVVVISAILA 540  
 Db 481 TYWEEQEPEVWSTLRLQVDRPLSVRCRLRNAGVQDTQEVIVVPHSLPFPKVVVISAILA 540  
 Qy 541 LVVLTIIISLIIILMLQKPRYIRKWVIESVSDGHEVIYVDPMLQPYDSTWELPRDOL 600  
 Db 541 LVVLTIIISLIIILMLQKPRYIRKWVIESVSDGHEVIYVDPMLQPYDSTWELPRDOL 600  
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 Db 601 VLGRITLGSAGFGQVATAGHLSHQATWKVAVMLKSTARSSEKQALMSELKIMSHLGP 660  
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 Db 661 HLMVNLGLACTGGPIYIITEYCRYGDLVDYLHRRNKHTFLQHSDDRPPPSAELYSNAL 720  
 Qy 721 PVGLPLPSHVSLSLGEDGGYMDSKDESVDYVPMIDMKGDVKYADIESNYNAPYDNYVP 780  
 Db 721 PVGLPLPSHVSLSLGEDGGYMDSKDESVDYVPMIDMKGDVKYADIESNYNAPYDNYVP 780  
 Qy 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLI CEGKLV 840  
 Db 781 SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLI CEGKLV 840  
 Qy 841 KICDFGLARDIMRDSNYISKGSTFPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
 Db 841 KICDFGLARDIMRDSNYISKGSTFPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
 Qy 901 GTPYPELPWNEQFYNAIKGYRNAQPAHASDEIYEMQKWEKFEIRPPFSQVLVLLER 960  
 Db 901 GTPYPELPWNEQFYNAIKGYRNAQPAHASDEIYEMQKWEKFEIRPPFSQVLVLLER 960  
 Qy 961 LLGEGYKKYQQVDEBFRLSDHPAILRSQARLPFGHLSRPLDTSVLYTAVQPNEGDND 1020  
 Db 961 LLGEGYKKYQQVDEBFRLSDHPAILRSQARLPFGHLSRPLDTSVLYTAVQPNEGDND 1020  
 Qy 1021 YIIPDPKPVEADEGFLSGSPSLASTNLNVENTSTISCDSPLEPQDEPEPQLEQV 1080  
 Db 1021 YIIPDPKPVEADEGFLSGSPSLASTNLNVENTSTISCDSPLEPQDEPEPQLEQV 1080  
 Qy 1081 EPEPELEQLPDSCCPAPRAEADSFL 1106  
 Db 1081 EPEPELEQLPDSCCPAPRAEADSFL 1106

RESULT 10

ABG72458

ID ABG72458 standard; protein; 1106 AA.

XX AC ABG72458;

XX DT 13-FEB-2003 (first entry)  
 XX DE Human platelet derived growth factor receptor beta mutant D826N.  
 XX KW Human; platelet derived growth factor receptor beta; PDGFRbeta;  
 KW hepatotropic; dermatological; nephrotropic; vulnary; ophthalmological;  
 KW cytosolic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;  
 KW phospholipase-inhibitor-C; receptor tyrosine kinase; cell proliferation;  
 KW cell migration; extracellular matrix synthesis; secretion;  
 KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;  
 KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;  
 KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;  
 XX mutant; mutin.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 OS XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..32  
 FT Protein /label= Signal\_peptide  
 FT /label=.1106  
 FT Domain /label= Mature\_PDGR\_beta  
 FT /label=.298  
 FT Domain /label= Immunoglobulin-like\_domain  
 FT /label=.398  
 FT Domain /label= Immunoglobulin-like\_domain  
 FT /label=.556  
 FT Domain /label= Transmembrane\_domain  
 FT /label=.694  
 FT Domain /note= "Split tyrosine kinase domain segment 1"  
 FT /note=.799..951  
 FT Domain /note= "Split tyrosine kinase domain segment 2"  
 FT Misc-difference 826  
 FT /note= "wild type Asp substituted by Asn"  
 XX US2002111304-A1.  
 PN 15-AUG-2002.  
 XX PD 25-MAY-2001; 2001US-00866510.  
 XX PF 01-DEC-2000; 2000US-0250747P.  
 PR 07-MAY-2001; 2001US-0289103P.  
 XX (KAZL/) KAZLAUSKAS A.  
 PA (IKUN/) IKUNO Y.  
 XX Kazlauskas A, Ikuno Y;  
 XX WPI: 2003-066697/06.  
 DR N-PSDB; ABS57789.  
 XX  
 PS Claim 7; Page 95-97; 127pp; English.  
 XX The invention describes a polypeptide comprising a portion of the  
 CC receptor tyrosine kinase platelet-derived growth factor alpha receptor  
 CC (PDGFalpha). The polypeptide and the polynucleotide are useful in  
 CC treating or preventing diseases and conditions associated with an  
 CC abnormal PDGF level or response, such as cell proliferation, cell  
 CC migration, extracellular matrix synthesis and secretion or cell  
 CC contraction. Exemplary diseases or disorders include cell proliferative  
 CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.  
 CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,  
 CC scleroderma, keloids, hypertrophic scars, skin wound healing or  
 CC proliferative vitreoretinopathy). The method may be used in identifying  
 CC compounds for treating or preventing the development of diseases  
 CC involving cell contraction, e.g. fibrotic diseases. This is the amino

CC	acid sequence of human platelet derived growth factor receptor (PDGFR)	
CC	beta mutant D826N	
XX		
SQ	Sequence 1106 AA;	
	Query Match 99.8%; Score 5757; DB 6; Length 1106;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 1104; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MRLPGAMPALAKGELLSSLLLELPQISQGLVVTTPGPELVNVSSTFVLTCSSAPV 60	961 LLGEGYKKYQVDEBFLRSDHPAILRQARLPGFHGLRSPDTSVLTAVQPNEGDND 1020
DB	1 MRLPGAMPALAKGELLSSLLLELPQISQGLVVTTPGPELVNVSSTFVLTCSSAPV 60	961 LLGEGYKKYQVDEBFLRSDHPAILRQARLPGFHGLRSPDTSVLTAVQPNEGDND 1020
QY	61 VMERMSQEPPEMAKADQGTFFSVLTLTNLGLDTGEYFCTHNSRGLTDERKRLYIFV 120	1021 YIIPLPDPKPEVADSGPLSGSLASSTLNEVNTSTISCDSPLFQDPEPEPEQLELQV 1080
DB	61 VMERMSQEPPEMAKADQGTFFSVLTLTNLGLDTGEYFCTHNSRGLTDERKRLYIFV 120	1021 YIIPLPDPKPEVADSGPLSGSLASSTLNEVNTSTISCDSPLFQDPEPEPEQLELQV 1080
QY	121 PDPVTGFLNDABELFIFLITEITIPCRVTDLPQLVVTLHEKKGDAVALPVPYDHORGFS 180	1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
DB	121 PDPVTGFLNDABELFIFLITEITIPCRVTDLPQLVVTLHEKKGDAVALPVPYDHORGFS 180	1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
QY	181 GFEDRSYICKTTIGREVSDSDAYVYRQVSSINVSNAVQTVVRQGENITLMCIIVGN 240	
DB	181 GFEDRSYICKTTIGREVSDSDAYVYRQVSSINVSNAVQTVVRQGENITLMCIIVGN 240	
QY	241 DVVNPEWTPRKESGRLEVPVTDFLDMPYHRSILHIPSALIEDSGTYTCNVTESVNDH 300	
DB	241 EVVNPEWTPRKESGRLEVPVTDFLDMPYHRSILHIPSALIEDSGTYTCNVTESVNDH 300	
QY	301 QDEKAINITVBSGYVRLLEGEVGTLOFAPLHRSRTLOVVFPEAYPPPTVLFWKDNRTLGDS 360	
DB	301 QDEKAINITVBSGYVRLLEGEVGTLOFAPLHRSRTLOVVFPEAYPPPTVLFWKDNRTLGDS 360	
QY	361 SAGEIALSRNSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVLQSLFQQLINVPVRVL 420	
DB	361 SAGEIALSRNSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVLQSLFQQLINVPVRVL 420	
QY	421 ELSSEHPDSEGTQVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480	
DB	421 ELSSEHPDSEGTQVRCRGRGMPQPNIIWSACRDLKRCPRELPTLLGNSSEESQLETVN 480	
QY	481 TYWEEBQEFVSTLRLQVDRPLSVRCRLRNAGQDQEVIVPHSLPFPKVVVISAILA 540	
DB	481 TYWEEBQEFVSTLRLQVDRPLSVRCRLRNAGQDQEVIVPHSLPFPKVVVISAILA 540	
QY	541 LVVLTTIISLIILMLQKKPRYIRWKVJESVSSDGHGHEIYVDPMPOLPYDSTWELPRDQL 600	
DB	541 LVVLTTIISLIILMLQKKPRYIRWKVJESVSSDGHGHEIYVDPMPOLPYDSTWELPRDQL 600	
QY	601 VLGRITLGSAGFGQVVBATAHGLSHSQATMKVAVYMLKSTARSSEKQALMSELKIMSHLGP 660	
DB	601 VLGRITLGSAGFGQVVBATAHGLSHSQATMKVAVYMLKSTARSSEKQALMSELKIMSHLGP 660	
QY	661 HLNVNLLGACTGGPIIYITEYCRVGDVLYLHRNKHTFLQHSKDRPPPSAELYSNAL 720	
DB	661 HLNVNLLGACTGGPIIYITEYCRVGDVLYLHRNKHTFLQHSKDRPPPSAELYSNAL 720	
QY	721 PVGLPLPSHVSULTGESDGGYMDMSKDSYDVYVPMLDKMGDKVYADIESNNYMAPYDNYVP 780	
DB	721 PVGLPLPSHVSULTGESDGGYMDMSKDSYDVYVPMLDKMGDKVYADIESNNYMAPYDNYVP 780	
QY	781 SAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICSGKLV 840	
DB	781 SAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICSGKLV 840	
QY	841 KICDFGLARDINRDSNYISKGSTFLPLKWNAPSIIFNSLYTTLSDVMSFGILLWEIFTLG 900	
DB	841 KICDFGLARDINRDSNYISKGSTFLPLKWNAPSIIFNSLYTTLSDVMSFGILLWEIFTLG 900	
QY	901 GTPYPPLPNEQFYNAIKGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLLLLER 960	
DB	901 GTPYPPLPNEQFYNAIKGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLLLLER 960	
QY		961 LLGEGYKKYQVDEBFLRSDHPAILRQARLPGFHGLRSPDTSVLTAVQPNEGDND 1020
DB		961 LLGEGYKKYQVDEBFLRSDHPAILRQARLPGFHGLRSPDTSVLTAVQPNEGDND 1020
QY		1021 YIIPLPDPKPEVADSGPLSGSLASSTLNEVNTSTISCDSPLFQDPEPEPEQLELQV 1080
DB		1021 YIIPLPDPKPEVADSGPLSGSLASSTLNEVNTSTISCDSPLFQDPEPEPEQLELQV 1080
QY		1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
DB		1081 EPEPELEQLPDSGCPAPRAEADSFL 1106
RESULT 11		
ABG72457		
ID	ABG72457 standard; protein; 1106 AA.	
XX		
AC	ABG72457;	
XX		
DT	13-FEB-2003 (first entry)	
XX		
DE	Human platelet derived growth factor receptor beta mutant T672M.	
XX		
KW	Human; platelet derived growth factor receptor beta; PDGFRbeta;	
KW	hepatotropic; dermatological; nephrotropic; vulnary; ophthalmological;	
KW	cytostatic; gene therapy; vaccine; phosphoinositide-kinase-inhibitor-3;	
KW	phospholipase-inhibitor-C; receptor tyrosine kinase; cell proliferation;	
KW	cell migration; extracellular matrix synthesis; secretion;	
KW	cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;	
KW	liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;	
KW	kelloid; hypertrophic scar; wound; proliferative vitreoretinopathy;	
KW	mutant; muten.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..32
FT		/label= Signal_peptide
FT	Protein	33..1106
FT		/label= Mature_PDGFR_beta
FT	Domain	227..298
FT		/label= Immunoglobulin-like_domain
FT	Domain	335..398
FT		/label= Immunoglobulin-like_domain
FT	Domain	532..556
FT		/label= Transmembrane_domain
FT	Domain	604..694
FT		/note= "Split tyrosine kinase domain segment 1"
FT	Misc-difference 672	/note= "wild type Thr substituted by Met"
FT		799..951
FT	Domain	/note= "Split tyrosine kinase domain segment 2"
FT		
XX		
PN	US2002111304-A1.	
XX		
PD	15-AUG-2002.	
XX		
XX	25-MAY-2001; 2001US-00866510.	
PF		
XX	01-DEC-2000; 2000US-0250747P.	
PR	07-MAY-2001; 2001US-0289103P.	
XX		
XX	(KAZL/) KAZLAUSKAS A.	
PA	(IKUN/) IKUNO Y.	
XX		
PI	Kazlauskas A, Ikuno Y;	
XX		
DR	WPI; 2003-066697/06.	
DR	N-PSDB; ABS57788.	
XX		
PT	New polypeptide for treating or preventing diseases associated with an abnormal platelet-derived growth factor (PDGF) level, e.g. cell	

PT	proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha or -beta.	
XX		
PS	Claim 7; Page 88-91; 127pp; English.	
XX		
CC	The invention describes a polypeptide comprising a portion of the receptor tyrosine kinase platelet-derived growth factor alpha receptor (PDGFalpha). The polypeptide and the polynucleotide are useful in treating or preventing diseases and conditions associated with an abnormal PDGF level or response, such as cell proliferation, cell migration, extracellular matrix synthesis and secretion or cell contraction. Exemplary diseases or disorders include cell proliferative diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g. atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis, scleroderma, keloids, hypertrophic scars, skin wound healing or proliferative vitreoretinopathy). The method may be used in identifying compounds for treating or preventing the development of diseases involving cell contraction, e.g. fibrotic diseases. This is the amino acid sequence of human platelet derived growth factor receptor (PDGFR) beta mutant T672M	
XX		
SQ	Sequence 1106 AA;	
	Query Match 99.8%; Score 5756; DB 6; Length 1106;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 1104; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	1 MRLPGAMPALAKGELLSSLLSLLLPQISQGLVTPPGPELVNLVNSFTVLTCSAPV 60	
DB	1 MRLPGAMPALAKGELLSSLLSLLLPQISQGLVTPPGPELVNLVNSFTVLTCSAPV 60	
QY	61 VVERMSQEPPOEMAKAQDGFSSVLTLTNLTGDTGEYFCTHNDSGLETDERKRLYIFV 120	
DB	61 VVERMSQEPPOEMAKAQDGFSSVLTLTNLTGDTGEYFCTHNDSGLETDERKRLYIFV 120	
QY	121 PDPTVGLFNDABEELFIFLTEITEITPCRVTPDQLVLTLEHKKGDVALPVPYDHQGRFS 180	
DB	121 PDPTVGLFNDABEELFIFLTEITEITPCRVTPDQLVLTLEHKKGDVALPVPYDHQGRFS 180	
QY	181 GIFEDRSYCKTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIIVGN 240	
DB	181 GIFEDRSYCKTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIIVGN 240	
QY	241 DVNPFETVPKESGRVLPVPTDFLMDPVRHSILHIPSAELEDGTYTCNVTESVNDH 300	
DB	241 EVNPFETVPKESGRVLPVPTDFLMDPVRHSILHIPSAELEDGTYTCNVTESVNDH 300	
QY	301 QDEKAINITVBSGYVRLLEGEVGTLOFABELHRSRTLQVVFAYPPPTVLWFKDNRITLGD 360	
DB	301 QDEKAINITVBSGYVRLLEGEVGTLOFABELHRSRTLQVVFAYPPPTVLWFKDNRITLGD 360	
QY	361 SAGEIALSRNVSSETRYSSELTLVRVKVAEAGHYTWRAFHEDAEVQLSFQLQINVPVRL 420	
DB	361 SAGEIALSRNVSSETRYSSELTLVRVKVAEAGHYTWRAFHEDAEVQLSFQLQINVPVRL 420	
QY	421 ELSSEHPDGEOTVRCRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETVN 480	
DB	421 ELSSEHPDGEOTVRCRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQLETVN 480	
QY	481 TYWEEQEFEVWSTLRQLQVDRPLSVRCITLRNAVGDQTOEIVVPHSLPFFKVVVISAILA 540	
DB	481 TYWEEQEFEVWSTLRQLQVDRPLSVRCITLRNAVGDQTOEIVVPHSLPFFKVVVISAILA 540	
QY	541 LVVLTITISILITLMQKPRYKIRWVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600	
DB	541 LVVLTITISILITLMQKPRYKIRWVIESVSSDGHYIYVDPMLPYDSTWELPRDQL 600	
QY	601 VLGRITLGSAGFGQVVEATAGHLSHSQATMKVAVKMLKSTARSEKQALMSELKINSHLGP 660	
DB	601 VLGRITLGSAGFGQVVEATAGHLSHSQATMKVAVKMLKSTARSEKQALMSELKINSHLGP 660	
QY	661 HLNVNLLGACTKGPIIYITEYCRYGDLVDYLHRNKHTFLQHSDKRPPPSAELYSNAL 720	
DB	661 HLNVNLLGACMKGPIIYITEYCRYGDLVDYLHRNKHTFLQHSDKRPPPSAELYSNAL 720	
QY	721 PVGLPLPSHVSITGESDGGYMDMSKDESVDYVPMGLMDKGDVYADIESSNYAPYDNYVP 780	
DB	721 PVGLPLPSHVSITGESDGGYMDMSKDESVDYVPMGLMDKGDVYADIESSNYAPYDNYVP 780	
QY	781 SAPERTCRATLINESPVLISYMDLVGFSYOVANGMEFLASKNCVHRDLAARNVLICBGLV 840	
DB	781 SAPERTCRATLINESPVLISYMDLVGFSYOVANGMEFLASKNCVHRDLAARNVLICBGLV 840	
QY	841 KICDFGLARDIMRDSNYISKGSTFLPLKWPAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900	
DB	841 KICDFGLARDIMRDSNYISKGSTFLPLKWPAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900	
QY	901 GTPYPELPMNEQFYNAIKRGYMAQFAHASDIYIEMQKWEKEFIRPPFSQLVLLER 960	
DB	901 GTPYPELPMNEQFYNAIKRGYMAQFAHASDIYIEMQKWEKEFIRPPFSQLVLLER 960	
QY	961 LLGEGYKKYQVDEEFLRSHPAILRSOARLPFGHLRSPLDTSSVLYTAVQPNEGDND 1020	
DB	961 LLGEGYKKYQVDEEFLRSHPAILRSOARLPFGHLRSPLDTSSVLYTAVQPNEGDND 1020	
QY	1021 YIIPLPDPKPEVADEGLESPSLASSTILNEVNTSTISCDSPLEPQDEPEPEPQLEQV 1080	
DB	1021 YIIPLPDPKPEVADEGLESPSLASSTILNEVNTSTISCDSPLEPQDEPEPEPQLEQV 1080	
QY	1081 EPEPELEQLPDGSCCAPRAEADSFL 1106	
DB	1081 EPEPELEQLPDGSCCAPRAEADSFL 1106	
XX	RESULT 12	
AB084677	ID AB084677 standard; protein; 1107 AA.	
XX	AB084677;	
AC	XX	
XX	XX	
DT	18-NOV-2004 (first entry)	
XX	XX	
DE	Human cancer-associated protein HP20-018.1.	
XX	XX	
KW	Human; cancer-associated protein; cytostatic; cancer; leukaemia;	
KW	Lymphoma; CAP.	
OS	Homo sapiens.	
XX	XX	
FN	WO2004074320-A2.	
XX	XX	
PD	02-SEP-2004.	
XX	XX	
PF	17-FEB-2004; 2004WO-US004730.	
XX	XX	
PR	14-FEB-2003; 2003US-00367094.	
PR	14-MAR-2003; 2003US-00388838.	
PR	15-APR-2003; 2003US-00417375.	
PR	13-JUN-2003; 2003US-00461862.	
PR	15-SEP-2003; 2003US-00663431.	
PR	15-DEC-2003; 2003US-00737318.	
XX	(SAGR-) SAGRES DISCOVERY INC.	
PA	Morris DW, Morris DW, Malandro MS;	
PI	WPI; 2004-652914/53.	
DR	N-PSDB; ABD32963.	
XX	XX	
PT	New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.	
XX	claim 18; seqid 706; 310pp; English.	
XX	The invention relates to an isolated nucleic acid comprising at least 10	

contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancer-associated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above recombinant nucleic acid or expression vector, a microarray for detecting a cancer-associated (CA) nucleic acid comprising at least one probe comprising at least 10 contiguous nucleotides of any of the above-mentioned nucleotide sequences, an isolated polypeptide (encoded within an open reading frame of a CA sequence selected from any of the 95 polynucleotide sequences as mentioned in the specification, or its complement), an isolated antibody, (or its antigen binding fragment) that binds to the above polypeptide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above antibody and a pharmaceutical excipient, a kit for detecting cancer cells (comprising the antibody cited above, methods for diagnosing cancer or for detecting the presence or absence of cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, a method for delivering a therapeutic agent to cancer cells in an individual, an electronic library comprising the above polynucleotide or polypeptide (or their fragments), methods of screening for anticancer activity or for a bioactive agent capable of modulating the activity of a CA protein (CAP), methods for detecting cancer associated with expression of a polypeptide in a test cell sample, a method for treating cancers and a method for inhibiting the expression of CA gene in a cell. The composition and methods are useful for detecting, diagnosing, preventing and treating cancers, especially lymphoma and leukaemia. These may also be used in screening for agents that modulate cancer. The present sequence is a human CAP protein sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 1107 AA;

Query Match 99.6%; Score 5745.5; DB 8; Length 1107;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1104; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MRLPGAMPALAKGELLALLSLLLELPQISQGLVVTTPPGPELVNVSSTFVLTCGSAV 60  
DB 1 MRLPGAMPALAKGELLALLSLLLELPQISQGLVVTTPPGPELVNVSSTFVLTCGSAV 60  
QY 61 VNERMSQEPPEQMAKAQDQTFSSVLTNLTLGLDGTGEYFCTHNDNRGLTDERKRLYIFV 120  
DB 61 VNERMSQEPPEQMAKAQDQTFSSVLTNLTLGLDGTGEYFCTHNDNRGLTDERKRLYIFV 120  
QY 121 PPTVGVFLPNDAAELFIFLITEITIPCRVTDPLQVLTILHEKKGVALPVYDHRGFS 180  
DB 121 PPTVGVFLPNDAAELFIFLITEITIPCRVTDPLQVLTILHEKKGVALPVYDHRGFS 180  
QY 181 GIFEDRSYICKTTIGDREVDSDAYVYRVLQVSSINVSNAVOTVVRQGENITLMCIIVGN 240  
DB 181 GIFEDRSYICKTTIGDREVDSDAYVYRVLQVSSINVSNAVOTVVRQGENITLMCIIVGN 240  
QY 241 DVNFEWTPYRKE-SGRUVEPVTFDILLDPYHRSILHIPSAALEDSGYTCNVTVSVD 299  
DB 241 EVNFEWTPYRKEVIGRLVEPVTFDILLDPYHRSILHIPSAALEDSGYTCNVTVSVD 300  
QY 300 HODEKAINITVVSQVRLGEGVTLOFAELHRSRTLQVFEAYPPTVLMFKDNRITLGD 359  
DB 301 HODEKAINITVVSQVRLGEGVTLOFAELHRSRTLQVFEAYPPTVLMFKDNRITLGD 360  
QY 360 SSAGEIALSTRNVSETRYVSELTLVRKVAEAGHYTMRAFHEDAEVQLSFQIQINPVVRV 419  
DB 361 SSAGEIALSTRNVSETRYVSELTLVRKVAEAGHYTMRAFHEDAEVQLSFQIQINPVVRV 420  
QY 420 LELSSHPDGSQGTVCRCRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSSEESQLETN 479  
DB 421 LELSSHPDGSQGTVCRCRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSSEESQLETN 480  
QY 480 VTYWEEQEFVYSTLRLOHVRPLSVRCTLRNAVQDQTEVIVVPHSLPFKVVVISAIL 539  
DB 481 VTYWEEQEFVYSTLRLOHVRPLSVRCTLRNAVQDQTEVIVVPHSLPFKVVVISAIL 540

QY 540 ALVVLTIISLIILMLQKKPRYEIRWKVIESVSDGHEIYVDPMLQPYDSTWELPRDQ 599  
DB 541 ALVVLTIISLIILMLQKKPRYEIRWKVIESVSDGHEIYVDPMLQPYDSTWELPRDQ 600  
QY 600 LVLGRTLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSELKIMSHLG 659  
DB 601 LVLGRTLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSELKIMSHLG 660  
QY 660 PHLVNVLGACTKGGPIYIITEYCRYGDLVDVYLHNKHTFLOHSDKRRPPSAEYLSNA 719  
DB 661 PHLVNVLGACTKGGPIYIITEYCRYGDLVDVYLHNKHTFLOHSDKRRPPSAEYLSNA 720  
QY 720 LPVGLPLPSHVSILTESDGGYMDSKDESVDYVPMMDKGDVKYADIESNNYMAPYDNYV 779  
DB 721 LPVGLPLPSHVSILTESDGGYMDSKDESVDYVPMMDKGDVKYADIESNNYMAPYDNYV 780  
QY 780 PSAPERTCRATLINESPVLSYMDLVGFYSQVANGMEFLASKKNCVHRDLAARNVLI CEGKL 839  
DB 781 PSAPERTCRATLINESPVLSYMDLVGFYSQVANGMEFLASKKNCVHRDLAARNVLI CEGKL 840  
QY 840 VKICDPLGLARDIMRDSNYISKGSTPLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTL 899  
DB 841 VKICDPLGLARDIMRDSNYISKGSTPLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTL 900  
QY 900 GGTYPPELPMNQFYNAIKRGYRMAQPAHASDEIYIMQKWEKFEIRPPFSQVLVLE 959  
DB 901 GGTYPPELPMNQFYNAIKRGYRMAQPAHASDEIYIMQKWEKFEIRPPFSQVLVLE 960  
QY 960 RLLGEGYKKYQOVDEEFLRSDHPAILRSQARLPGFHGLRSLDTSVLYTAVQPNEGDN 1019  
DB 961 RLLGEGYKKYQOVDEEFLRSDHPAILRSQARLPGFHGLRSLDTSVLYTAVQPNEGDN 1020  
QY 1020 DVIILPDPKPEVADEGPLEGSPSLASSTLNEVTSSTISCDSPLEPQDEPEPEPELEQ 1079  
DB 1021 DVIILPDPKPEVADEGPLEGSPSLASSTLNEVTSSTISCDSPLEPQDEPEPEPELEQ 1080  
QY 1080 VEPELEQLPDSGCPAPRAEADSFL 1106  
DB 1081 VEPELEQLPDSGCPAPRAEADSFL 1107  
RESULT 13  
AAP90646  
ID AAP90646 standard; protein; 1106 AA.  
XX AAP90646;  
AC AAP90646;  
XX 24-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 20-OCT-1989 (first entry)  
XX  
DE Human platelet-derived growth factor receptor.  
XX Human platelet derived growth factor receptor;  
KW agonist and antagonist drugs; wound healing; prevents atherosclerosis;  
KW cancer; genetic disorders; antibodies.  
XX  
OS Homo sapiens; (human).  
XX  
FH Key Location/Qualifiers  
FT Region 45..47  
FT Region 89..91  
FT Region 103..105  
FT Region 215..217  
FT Region 230..232  
FT Region 292..294  
FT Region 307..309  
FT Region 354..356  
FT Region 371..373  
FT Region 468..470  
FT Region 479..481  
FT Domain 531..555

XX EP327369-A.  
XX 09-AUG-1989.  
XX 02-FEB-1989; 89EP-00301021.  
XX 02-FEB-1989; 88US-00151414.  
XX (REGC ) UNIV CALIFORNIA.  
XX Williams LT, Escobedo JE;  
XX WPI; 1989-229378/32.  
XX New DNA encoding human platelet derived growth factor receptor - useful  
XX e.g. for assessing agonist and antagonist drugs.  
XX Claim 1; Page 3; 12pp; English.  
XX Human platelet derived growth factor receptor (see AAN90388) for  
XX features). Used to make probes and antibodies, and to evaluate drugs. The  
XX regions specified are potential N-glycosylation sites, and the domain is  
XX a transmembrane sequence. (Updated on 25-MAR-2003 to correct PA field.)  
XX (Updated on 24-OCT-2003 to standardise OS field)  
XX SQ Sequence 1106 AA;  
Query Match 98.7%; Score 5691; DB 1; Length 1106;  
Best Local Similarity 98.6%; Pred. No. 0;  
Matches 1091; Conservative 9; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MRLPGAMPALAKGELLSSLLLELPQISQGLVTPPGPELVNLVNSSTFVLTCGSAFV 60  
DB 1 MRLPGAMPALAKGELLSSLLLELPQISQGLVTPPGPELVNLVNSSTFVLTCGSAFV 60  
QY 61 VNERMSQEPQEMAKAQDGFSSVLTNLTLGLTGEYFCTHNDRGLDTERKRLYIFV 120  
DB 61 VNERMSQEPQEMAKAQDGFSSVLTNLTLGLTGEYFCTHNDRGLDTERKRLYIFV 120  
QY 121 PPTVGVFLNDABEELFIFLITEITIPCRVTDPLQVLTLEHKKGDVALPVPYDHQGRFS 180  
DB 121 PPTVGVFLNDABEELFIFLITEITIPCRVTDPLQVLTLEHKKGDVALPVPYDHQGRFS 180  
QY 181 GIPEDRSYICKTIGREVDSDAYVYRLQVSSINVSNAVQTVRQGENITLVCIVGN 240  
DB 181 GIPEDRSYICKTIGREVDSDAYVYRLQVSSINVSNAVQTVRQGENITLVCIVGN 240  
QY 241 DVNFEWTPRKESGRLEVPVTDPLDMPYHRSILHIPSALIEDSGTYTCNVTSVNDH 300  
DB 241 EVNFEWTPRKESGRLEVPVTDPLDMPYHRSILHIPSALIEDSGTYTCNVTSVNDH 300  
QY 301 QDEKAINITVQSGYVRLLEGEVTLQFAELHRSRTLQVFEAYPPPTVLWFKDNRTLGD 360  
DB 301 QDEKAINITVQSGYVRLLEGEVTLQFAELHRSRTLQVFEAYPPPTVLWFKDNRTLGD 360  
QY 361 SAGEIALSTRNVSETRYVSELTLVRVKAAGHYTWRAHEDAEVQLSFQQLNVPRVL 420  
DB 361 SAGEIALSTRNVSETRYVSELTLVRVKAAGHYTWRAHEDAEVQLSFQQLNVPRVL 420  
QY 421 ELSEHPDSCGEQVRCRGMQPNIIWSACRDLKRCPRPLPTLLGNSSEESQLETVN 480  
DB 421 LLESHPDSCGEQVRCRGMQPNIIWSACRDLKRCPRPLPTLLGNSSEESQLETVN 480  
QY 481 TYWEEQEFVSTRLQHVDRPLSVRCTLNVAVGQDTQEVIVVPHSLPKVVI SAILA 540  
DB 481 TYWEEQEFVSTRLQHVDRPLSVRCTLNVAVGQDTQEVIVVPHSLPKVVI SAILA 540  
QY 541 LVVLTIISLILMLWQKPKRYEIRWKVIESVSDGHEIYVDPMPQYDSTWELPRDQL 600  
DB 541 LLLTITISLILMLWQKPKRYEIRWKVIESVSDGHEIYVDPMPQYDSTWELPRDQL 600  
QY 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660

DB 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660  
QY 661 HLNVNLLGACTKGGPIYITEYCRYGDLVDYLHRNKHTEFLOHSDKRRPPSAEYLSNAL 720  
DB 661 HLNVNLLGACTKGGPIYITEYCRYGDLVDYLHRNKHTEFLOHSDKRRPPSAEYLSNAL 720  
QY 721 PVGLPLSHVSLTGESDGYMDMSKDSVDVPMMDKMDGVKYADIESSNMAPYDNYVP 780  
DB 721 PVGLPLSHVSLTGESDGYMDMSKDSVDVPMMDKMDGVKYADIESSNMAPYDNYVP 780  
QY 781 SAPERTCRATLINESPVLSYMDLVGFYSQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840  
DB 781 SAPERTCRATLINESPVLSYMDLVGFYSQVANGMEFLASKNCVHRDLAARNVLICEGKLV 840  
QY 841 KICDFGLARDIMRASNYISKSTFLPLKMAPEISFNSLYTLSDVMSFGILLWEIFTLG 900  
DB 841 KICDFGLARDIMRASNYISKSTFLPLKMAPEISFNSLYTLSDVMSFGILLWEIFTLG 900  
QY 901 GTPPELPMNEOFYNAIKRGYRMAQPAHASDEIYEIMOKCWEKEFEIRPPFSQVLVLLER 960  
DB 901 GTPPELPMNEOFYNAIKRGYRMAQPAHASDEIYEIMOKCWEKEFEIRPPFSQVLVLLER 960  
QY 961 LLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPFGHGLRSPDTSVLYTAVQPNEGND 1020  
DB 961 LLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPFGHGLRSPDTSVLYTAVQPNEGND 1020  
QY 1021 YIILPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPELOLEQV 1080  
DB 1021 YIILPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEPEPELOLEQV 1080  
QY 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106  
DB 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106  
RESULT 14  
ABG72455  
ID ABG72455 standard; protein; 1090 AA.  
XX AC ABG72455;  
XX DT 13-FEB-2003 (first entry)  
XX Human platelet derived growth factor receptor beta.  
DE Human; platelet derived growth factor receptor alpha; PDGFRalpha;  
KW hepatotropic; dermatological; nephrotropic; vulnary; ophthalmological;  
KW cytosolic; gene therapy; vaccine; phosphoinositide-Kinase-inhibitor-3;  
KW phospholipase-inhibitor-C; receptor tyrosine kinase; cell proliferation;  
KW cell migration; extracellular matrix synthesis; secretion;  
KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;  
KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;  
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy.  
XX OS Homo sapiens.  
XX Key Location/Qualifiers  
XX Peptide 1..32  
FT /label= Signal\_peptide  
FT Protein 33..1106  
FT /label= Mature\_PDGFR\_beta  
FT Domain 227..298  
FT /label= Immunoglobulin-like\_domain  
FT Domain 335..398  
FT /label= Immunoglobulin-like\_domain  
FT Domain 532..556  
FT /label= Transmembrane\_domain  
FT Domain 604..694  
FT /note= "Split tyrosine kinase domain segment 1"  
FT 799..951  
FT /note= "Split tyrosine kinase domain segment 2"  
XX



[illegible]

Search completed: March 11, 2005, 07:07:45  
Job time : 134.495 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2005, 07:07:56 ; Search time 34.2633 Seconds  
(without alignments)  
3105.821 Million cell updates/sec

Title: US-10-027-400-4

Perfect score: 5766

Sequence: 1 MRLPGAMPALKGELLLS.....EQLPDGCPAPRAEDSFL 1106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5762	99.9	1106	1	PFHMRB
2	4972	86.2	1098	1	platelet-derived g
3	2403	41.7	1048	2	platelet-derived g
4	2351.5	40.8	1089	1	platelet-derived g
5	2319	40.2	1087	2	platelet-derived g
6	2304	40.0	1088	1	platelet-derived g
7	2271.5	39.4	1089	1	platelet-derived g
8	2115	36.7	499	2	platelet-derived g
9	1432.5	24.8	980	1	macrophage colony-
10	1425	24.7	978	1	protein-tyrosine k
11	1421.5	24.7	941	1	protein-tyrosine k
12	1401.5	24.3	960	1	protein-tyrosine k
13	1400.5	24.3	976	1	protein-tyrosine k
14	1384.5	24.0	977	2	protein-tyrosine k
15	1382.5	24.0	975	1	protein-tyrosine k
16	1382	24.0	978	2	macrophage colony-
17	1370.5	23.8	972	1	macrophage colony-
18	1355.5	23.5	976	1	c-kit-related kina
19	1327	23.0	954	2	macrophage colony-
20	1274	22.1	975	2	receptor tyrosine
21	1138	19.7	1333	2	vascular endotheli
22	1138	19.7	1379	2	Fit-1 tyrosine kin
23	1133.5	19.7	1336	2	platelet-derived g
24	1131.5	19.6	457	2	vascular endotheli
25	1115	19.3	1348	2	protein-tyrosine k
26	1105	19.2	1363	2	embryonic receptor
27	1100.5	19.1	1330	2	protein-tyrosine k
28	1099.5	19.1	1338	2	protein-tyrosine k
29	1095	19.0	1000	2	Flt3 protein - mou

#### ALIGNMENTS

##### RESULT 1

PFHUGB

platelet-derived growth factor receptor beta precursor - human  
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004

C/Accession: A28206; A31195; A38268; A31925; B31925; C31925

R:Gronwald, R.G.K.; Grant, F.J.; Haldeman, B.A.; Hart, C.E.; O'Hara, P.J.; Hagen, F.S.;

Proc. Natl. Acad. Sci. U.S.A. 85, 3435-3439, 1988

A>Title: Cloning and expression of a cDNA coding for the human platelet-derived growth f

A/Reference number: A28206; MUID:88217915; PMID:2835772

A/Accession: A28206

A/Molecule type: mRNA

A/Residues: 1-1106 <GRO>

A/Cross-references: UNIPROT:P09619; GB:J03278; GB:J03278; PID:G189731; PID:AAA60049.1; PID:G189732

R:Clackson-Welsh, L.; Eriksson, A.; Mollen, A.; Severinson, L.; Ek, B.; Oestman, A.; Bet

Mol. Cell. Biol. 8, 3476-3486, 1988

A>Title: cDNA cloning and expression of a human platelet-derived growth factor (PDGF) re

A/Reference number: A31195; MUID:89096941; PMID:2850496

A/Accession: A31195

A/Molecule type: mRNA

A/Residues: 1-240, 'D', 242-1106 <CLA>

A/Cross-references: GB:M21616; NID:G189729; PID:AAA36427.1; PID:G189730

R:Partanen, J.; Maelkel, T.P.; Alitalo, R.; Lehtvaeslaiho, H.; Alitalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A>Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A/Reference number: A38268; MUID:91062389; PMID:2247464

A/Accession: A38268

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 828-884 <PAR>

R:Roberts, W.M.; Look, A.T.; Rousset, M.P.; Sherr, C.J.

Cell 55, 555-561, 1988

A>Title: Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor genes.

A/Reference number: A90908; MUID:89028677; PMID:2846185

A/Accession: A31925

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 676-727 <ROB>

A/Accession: B31925

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 901-912 <RO2>

A/Accession: C31925

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1047-1106 <RO3>

C/Comment: The extracellular domain is predicted to include five immunoglobulin-like dom

A/Gene: GDB:PDGFRB

A/Cross-references: GDB:I20710; OMIM:173410

A/Map position: 5q31-5q32

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer;  
F;1-32/Domain: signal sequence #status predicted <SIG>  
F;33-1106/Product: platelet-derived growth factor receptor beta #status predicted <MAT>  
F;33-531/Domain: extracellular #status predicted <EXT>  
F;47-102/Domain: immunoglobulin homology <IMM1>  
F;142-192/Domain: immunoglobulin homology <IMM2>  
F;228-293/Domain: immunoglobulin homology <IMM3>  
F;429-510/Domain: immunoglobulin homology <IMM4>  
F;532-555/Domain: transmembrane #status predicted <TMW>  
F;556-1106/Domain: intracellular #status predicted <INT>  
F;598-965/Domain: protein kinase homology <KIN>  
F;606-614/Region: protein kinase ATP-binding motif  
F;45, 89, 103, 215, 230, 292, 307, 354, 371, 468, 479/Binding site: carbohydrate (Asn) (covalent)  
F;54-100, 149-190, 235-291, 436-508/disulfide bonds: #status predicted  
F;634/Active site: lys #status predicted  
F;857/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 99.9%; Score 5762; DB 1; Length 1106;  
Best Local Similarity 99.9%; Pred. No. 1.4e-248;  
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLPGAMPALAKGELLALLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCGSAVP 60  
Db 1 MRLPGAMPALAKGELLALLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCGSAVP 60

Qy 61 WERMSEPPQEMAKAQDGTFFSSVLTNLTLGLDTGEYFCTHNDNRGLTDERKRLYIFV 120  
Db 61 WERMSEPPQEMAKAQDGTFFSSVLTNLTLGLDTGEYFCTHNDNRGLTDERKRLYIFV 120

Qy 121 PDVTGFLPDNDELFLTEITITPCRVTPDQLVTLHEKKGDVALPVPVDHQRGFS 180  
Db 121 PDVTGFLPDNDELFLTEITITPCRVTPDQLVTLHEKKGDVALPVPVDHQRGFS 180

Qy 181 GIFEDRSYICKTIGDREVDSDAYVYVRLQVSSINVSNAVQTVRQENITLMCVIGN 240  
Db 181 GIFEDRSYICKTIGDREVDSDAYVYVRLQVSSINVSNAVQTVRQENITLMCVIGN 240

Qy 241 DVNPFNTYPRKSGRLVEPTDFLDMPYHRSILHIPSAAELDSGTTCNTVESVNDH 300  
Db 241 EVNPFNTYPRKSGRLVEPTDFLDMPYHRSILHIPSAAELDSGTTCNTVESVNDH 300

Qy 301 QDEKAINITVVEGYVRLLEGEVGLQPAELHRRTLQVPEAYPPPPVFLFKDNRITLGD 360  
Db 301 QDEKAINITVVEGYVRLLEGEVGLQPAELHRRTLQVPEAYPPPPVFLFKDNRITLGD 360

Qy 361 SAGEIALSTRNVSETRVYSELTLVRVKVABAGHYTWRAPFEDAEVQLSFQQLINVPVRVL 420  
Db 361 SAGEIALSTRNVSETRVYSELTLVRVKVABAGHYTWRAPFEDAEVQLSFQQLINVPVRVL 420

Qy 421 ELSHSDPSGEQVRCRGMPQNIITWSACDLKRCPCRELPTLLGNSEESQLETNV 480  
Db 421 ELSHSDPSGEQVRCRGMPQNIITWSACDLKRCPCRELPTLLGNSEESQLETNV 480

Qy 481 TYWEEQEFVWSTLRQLQHVDRPLSVRCTLRNAGVQDQTEVIVVPHSLPKVWVISAIA 540  
Db 481 TYWEEQEFVWSTLRQLQHVDRPLSVRCTLRNAGVQDQTEVIVVPHSLPKVWVISAIA 540

Qy 541 LVVLTISLILIMLWQKKPRYIRWKVIESVSDGHEIYVDPMQLPYDSTWELPRDQL 600  
Db 541 LVVLTISLILIMLWQKKPRYIRWKVIESVSDGHEIYVDPMQLPYDSTWELPRDQL 600

Qy 601 VLGRITLGSAGFGQVETAGHLSQNTKVMKVKSTARSSEKQALMSELKIMSHLGP 660  
Db 601 VLGRITLGSAGFGQVETAGHLSQNTKVMKVKSTARSSEKQALMSELKIMSHLGP 660

Qy 661 HLNVNLLGACTGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSKDRRPPSAELYSNAL 720  
Db 661 HLNVNLLGACTGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSKDRRPPSAELYSNAL 720

Qy 721 PVGLPLPSHVSLSLTCESDGYMDMSKDESVDYVPMMLDMKGVKYADIBSSNYMAPYDNYVP 780  
Db 721 PVGLPLPSHVSLSLTCESDGYMDMSKDESVDYVPMMLDMKGVKYADIBSSNYMAPYDNYVP 780

Qy 781 SAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGLV 840  
Db 781 SAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGLV 840

Qy 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900  
Db 841 KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900

Qy 901 GTPYPELPWNEQYNAIKRGYRMAQPAHASDEIYEIMQKWCBEKFEIRPPFSQVLVLLER 960  
Db 901 GTPYPELPWNEQYNAIKRGYRMAQPAHASDEIYEIMQKWCBEKFEIRPPFSQVLVLLER 960

Qy 961 LLGEGYKKYQVQVDEBFLRSDHPAILRQARLPGFHLRPLDTSSVLYTAVQPNEGDND 1020  
Db 961 LLGEGYKKYQVQVDEBFLRSDHPAILRQARLPGFHLRPLDTSSVLYTAVQPNEGDND 1020

Qy 1021 YIIPLPDPKPEVADEGLEGSPSLASSTLNEVNTSITSCDSPLEQDEPEPEPQLEQV 1080  
Db 1021 YIIPLPDPKPEVADEGLEGSPSLASSTLNEVNTSITSCDSPLEQDEPEPEPQLEQV 1080

Qy 1081 EPEPELEQLPDSGCCPAPRAEADSFL 1106  
Db 1081 EPEPELEQLPDSGCCPAPRAEADSFL 1106

RESULT 2  
PFMSRB  
N;Contains: growth factor receptor beta precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A25742  
R;arden, Y.; Escobedo, J.A.; Kuang, W.J.; Yang-Feng, T.L.; Daniel, T.O.; Tremble, P.M.;  
Nature 323, 226-232, 1996  
A;Title: Structure of the receptor for platelet-derived growth factor helps define a fam  
A;Reference number: A25742; MUID:87014762; PMID:3020426  
A;Accession: A25742  
A;Molecule type: mRNA  
A;Residues: 1-1098 <YAR>  
A;Cross-references: UNIPROT:P05622; EMBL:X04367; NID:g53618; PIDN:CAA27882.1; PID:g53619  
A;Note: part of this sequence, including the amino end of the mature protein, was confir  
C;Comment: The extracellular domain is predicted to include five immunoglobulin-like doma  
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer;  
F;1-31/Domain: signal sequence #status predicted <SIG>  
F;32-1098/Product: platelet-derived growth factor receptor beta #status predicted <MAT>  
F;32-530/Domain: extracellular #status predicted <EXT>  
F;46-101/Domain: immunoglobulin homology <IMM1>  
F;141-191/Domain: immunoglobulin homology <IMM2>  
F;227-292/Domain: immunoglobulin homology <IMM3>  
F;428-509/Domain: transmembrane #status predicted <TMW>  
F;531-554/Domain: intracellular #status predicted <INT>  
F;555-1098/Domain: intracellular #status predicted <INT>  
F;597-964/Region: protein kinase ATP-binding motif  
F;45, 89, 103, 214, 291, 306, 353, 370, 444, 467, 478/Binding site: carbohydrate (Asn) (covalent)  
F;53-99, 148-189, 234-290, 435-507/disulfide bonds: #status predicted  
F;633/Active site: lys #status predicted  
F;856/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.2%; Score 4972; DB 1; Length 1098;  
Best Local Similarity 85.4%; Pred. No. 1.6e-213;  
Matches 945; Conservative 76; Mismatches 77; Indels 8; Gaps 2;

Qy 1 MRLPGAMPALAKGELLALLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCGSAVP 60  
Db 1 MRLPGAMPALAKGELLALLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCGSAVP 59

Qy 61 WERMSEPPQEMAKAQDGTFFSSVLTNLTLGLDTGEYFCTHNDNRGLTDERKRLYIFV 120  
Db 61 WERMSEPPQEMAKAQDGTFFSSVLTNLTLGLDTGEYFCTHNDNRGLTDERKRLYIFV 119

121 PDPTGFLPNDABELFIFLITEITITPCRVTPDQLVVTLLHKKGDVALPVPYDHQGF 180  
 120 PDPTGFLPMDSDRLFVTDVTEITPCRVTPDQLVVTLLHKKGDVPLHVPYDHQGF 179  
 181 GIFEDRSYCKTTIGREVDSDAYVYVRLQVSSINVSNAVQTVRQGENITLVCIVGN 240  
 180 GTFEDKTYCKTTIGREVDSDTYVYVSLQVSSINVSNAVQTVRQGESITTCIVMGN 239  
 241 DVNPFMTYPRKESGRLEVPVTPDPLDMPYHRSILHIPSABELEDSTYTCNVTSVNDH 300  
 240 DVNPFMTYPRKESGRLEVPVTPDPLDMPYHRSILHIPSABELEDSTYTCNVTSVNDH 299  
 301 QDEKAINITVSGYVRLLEGEVGTQFAELHRSRTLQVFEAYPPPTVLMFKDNRILGDS 360  
 300 GDEKAINISVIENGYVRLLEGEVGTQFAELHRSRTLQVFEAYPPPTVLMFKDNRILGDS 359  
 361 SAGEIALSTRNVSETRYVSELTLVRUKVAAGHYTWRAPHEDEAVQLSPQLQNVPRVL 420  
 360 GAGELVLRNMSETRYVSELTLVRUKVAAGHYTWRAPHEDEAVQLSPQLQNVPRVL 419  
 421 ELSSEHPDSEQTVRCRGMPQPNIIWSACRDLKRCPRPLPTLLGNSSEESQLETVN 480  
 420 ELSSEHPDSEQTVRCRGMPQPNIIWSACRDLKRCPRPLPTLLGNSSEESQLETVN 479  
 481 TYWEEBQEFVWSTLRLQVHVDRLPVSRLTNRNAVQDQTVIIVPHSLPKVYVISAIA 540  
 480 TFWEDEQEVVSTLRLQVHVDRLPVSRLTNRNAVQDQTVIIVPHSLPKVYVISAIA 539  
 541 LVVLTITSLIILMLQKPRYRIRKVIKVSVDGHEIYVDPMLPYDSTWELPRDQL 600  
 540 LVVLTITSLIILMLQKPRYRIRKVIKVSVDGHEIYVDPMLPYDSTWELPRDQL 599  
 601 VLGRITLGSAGFQVQVATAGLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 660  
 600 VLGRITLGSAGFQVQVATAGLSHQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP 659  
 661 HLMNVNLLGACTGGPIIITTEYCRYGDLVDYLHKNKHTFLQHSKRRPPSAELYSNAL 720  
 660 HLMNVNLLGACTGGPIIITTEYCRYGDLVDYLHKNKHTFLQHSKRRPPSAELYSNAL 719  
 721 PVGLPLPSHVLTSGEDGGYMDMSKDESVDYVPMKMGDKVYKADISSNYMAPYDNYVP 780  
 720 PVGFLPSHLNLTGSDGGYMDMSKDESVDYVPMKMGDKVYKADISSNYMAPYDNYVP 779  
 781 SAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCVYHRDLAARNVLI 840  
 780 SAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCVYHRDLAARNVLI 839  
 841 KICDFGLARDIMRDSNYISKGSTFLPLKMWAPESIFNSLYTLLSDVMSFGILLWEIFTLG 900  
 840 KICDFGLARDIMRDSNYISKGSTFLPLKMWAPESIFNSLYTLLSDVMSFGILLWEIFTLG 899  
 901 GTPYPELPMEQYNAIKRGYMAQPAHASDEIYEMQKWEKFEIRPPPSQLVLLER 960  
 900 GTPYPELPMEQYNAIKRGYMAQPAHASDEIYEMQKWEKFEIRPPPSQLVLLER 959  
 961 LLEGYKXKYQVDEFLRSDHAILRSOARLPGFCLRSPLDTSVLYTAVOPNDSND 1020  
 960 LLEGYKXKYQVDEFLRSDHAILRSOARLPGFCLRSPLDTSVLYTAVOPNDSND 1019  
 1021 YIPLPDPKPEVADGEPLEGSPSLASTLNEVNTSSTICDSEPLEQPEPPQLEQLV 1080  
 1020 YIPLPDPKPEVADGEPLEGSPSLASTLNEVNTSSTICDSEPLEQPEPPQLEQLV 1072  
 1081 EPPELEQLPDSGCPAPRAEADSFL 1106  
 1073 EPPELEQLPDSGCPAPRAEADSFL 1098

RESULT 3  
 T30815  
 platelet-derived growth factor receptor beta - Japanese pufferfish

C:Species: Fugu rubripes (Japanese pufferfish)  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C:Accession: T30815  
 R:How, G.F.; Venkatesh, B.; Brenner, S.  
 Genome Res. 6, 1185-1191, 1996  
 A:Title: Conserved linkage between the pufferfish (Fugu rubripes) and human genes for pla  
 A:Reference number: Z20882; MUID:97129405; PMID:8973913  
 A:Accession: T30815  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1048 <HOW>  
 A:Cross-references: UNIPROT:P79749; EMBL:U63926; NID:gl752706; PID:gl752707; PIDN:AAC600  
 C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
 Query Match 41.7%; Score 2403; DB 2; Length 1048;  
 Best Local Similarity 48.5%; Pred. No. 1.7e-99;  
 Matches 518; Conservative 159; Mismatches 321; Indels 70; Gaps 18;  
 9 ALAKGELLLSL---LILLEPOISQGLVVTTPGPELVLNVSTFVLTCGSGAPVWERM 65  
 4 ASAMRAAVLHLTVALAALLSSCTTVSCLKIVPEKQLILAEGSSLSLTGAGSSETTWDLK 63  
 66 SQEPPQEMAKA-----QDGTFSVLTNLTLGLDTGEYFECTHNDSRGLETDERK 115  
 64 SDDVPFFQKAESSDLNFKIVOSNSTASVLTLMHVDKNTAVYQC-----REQLTGIKE 118  
 116 LVTFVDP---PTVGFPLPNDABELFLTEIT-EITPCRVTPDQLVVTLLHKKGDVALP 170  
 119 VAVFVDRSPQTLRFI---ESSHGMVTKSGESVPCVVTNPNITVLYDXDQTLDPVN 174  
 171 VPDYHQRGSGIFEDRSYICKTTIGREVDSDAYVYVRLQV-SSINVSNAVQTVRQGE 229  
 175 GVYVPSGFKAYLDYRTYVCRGELNGEVKESQAFNVYSIHVPEDIDAYVNASQTVLKQGE 234  
 230 NITLMCIVIGNDVNVFNTYPRKESGRLEVPVTPDPLDMPYHRSILHIPSABELEDSTY 289  
 235 PLTVNCTVGQVLELVFSDIPNRD---IVKHKPETVLVSATTMRSCLVFPFHTVAHSGTY 291  
 290 TCNVTSVNDHODEKAINITVSGYVRLLEGEVGTQFAELHRSRTLQVFEAYPPPTVL 349  
 292 VCHAESTQDQKAFASVNTVLERGFVAVKSTRKQNTAELQENVELRVEIEAYPPQIR 351  
 350 WFKONRTLDGSSAGEIALSTRNVSETRYVSELTLVRUKVAAGHYTWRAPHEDEAVQLSP 409  
 352 WKKD---GAPVRGDKTIIIRQHEIRYVTLTLVRVTEQKGLYALTITNEDDVKEVTF 407  
 410 QLOQINVPVRLVLESHSPDSGEQTVRCRGMPQPNIIWSACRDLKRCPRPLPTLLGNS 469  
 408 ALEVQVLARIKDLTDHHLFGKQLVTCVAEGVPTTIQWYSCDSMLKCNQTSMLWQOLKA 467  
 470 SEESOLETNVTWEEBQEFV---YSTLRQLQVDRPLSVRCVTRLNNAVGO-DTQEVIVVP 525  
 468 DELLSIHTSVT---EARQTNQVRSQVTFPKQHT---TVRCETTQEGGLIDFRDKVLVS 521  
 526 HSLPFKVVVISALALVLTITSLIILMLQKPRYRIRKVIKVSVDGHEIYVDPN 585  
 522 SLSFSQVLLAVVLTLPVPIIISIIILIAVKKKPRYRIRKVIKVSVDGHEIYVDPN 581  
 586 QLPYDSTWELPRDQLVGLRGLTSGAGFQVQVATAGLSHQATMKVAVKMLKSTARSSEK 645  
 582 HLPYDLAWEMPRDNLVGLRGLTSGAGFQVQVATAGLSHQATMKVAVKMLKSTARSSEK 641  
 646 QALMSLKTMHSLGPHLVNVLGACTGGPIIITTEYCRYGDLVDYLHKNKHTFLQHS 705  
 642 QALMSLKTMHSLGPHLVNVLGACTGGPIIITTEYCRYGDLVDYLHKNKHTFLQYL 701  
 706 DKRPPSAELYSNALPVGLPLPSHVLTSGEDGGYMDMSKDESVDYVPMKMGDKVYKAD 765  
 702 DRNQDDGSLISGGSTPLS-QRKGYVSGESDGGYMDMSKDEPAVYVPMQEQMDTIKYAD 760  
 766 IESSNTWAPY--DNYVPSAPERTCRATLINESPVLSTYMDLVGFSYQVANGMEFLASKNCV 823  
 761 IOPSPESYQDLYQEQGGGRV--DLVISDSPLTYDLDLLGFSYQVAKGMEFLASKNCV 818

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QY 824 HRDLAARNVLICGKLVKICDFGLARDIMRDSNVYISKGSTFLPLKMWAPESIFNSLYTTL 883
Db 819 HRDLAARNVLICGKLVKICDFGLARDIMRDSNVYISKGSTFLPLKMWAPESIFNSLYTTL 878
QY 884 SDVMSFGILLWEFTLGGTTPYLPPELMNEQFYNAIKRGYRMAQPAHASDEIYEMQKWEE 943
Db 879 SDVMSFGILLWEFTLGGTTPYLPPELMNEQFYNAIKRGYRMAQPAHASDEIYEMQKWEE 938
QY 944 KFEIRPPFSOLVLLERLLGEGYKKYQVDEBFLRSDHPAILRSQARLPGFHGLRSLD 1003
Db 939 TFEKRPDPFSLVHCVGDMLTDSYKKYSQVNETFLKSDHPAVARTKRLSSPPFIANPAF 998
QY 1004 TSSVLY-----TAVQNEGD-----NDYIILPLDPKPE 1031
Db 999 GSPSLVGLSDPDPYNQNTFRNEAEVQSGVTSFNEYIILPIDPKPE 1046

RESULT 4
PFHUGA
platelet-derived growth factor receptor alpha precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40162; A32941
R;Matuul, T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle, W.; Kraus, M.; Pierce, J
Science 243, 800-804, 1989
A;Title: Isolation of a novel receptor cDNA establishes the existence of two PDGF receptor
A;Reference number: A40162; MUID:89130149; PMID:2536956
A;Accession: A40162
A;Molecule type: mRNA
A;Residues: 1-1089 <MATS>
A;Cross-references: UNIPROT:P16234; GB:M21574; NID:g189733; PIDN:AAA96715.1; PID:g189734
R;Claesson-Welsh, L.; Eriksson, A.; Westermark, B.; Heidun, C.H.
Proc. Natl. Acad. Sci. U.S.A. 86, 4917-4921, 1989
A;Title: cDNA cloning and expression of the human A-type platelet-derived growth factor
A;Reference number: A32941; MUID:89296915; PMID:2544881
A;Accession: A32941
A;Molecule type: mRNA
A;Residues: 1-1089 <CIA>
A;Cross-references: GB:M22734; NID:g189725; PIDN:AAA60048.1; PID:g189726
C;Comment: The extracellular domain is predicted to include five immunoglobulin-like dom
C;Genetics:
A;Gene: GDB:PDGFRA
A;Cross-references: GDB:120267; OMIM:173490
A;Map position: 4q11-q12
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; autophosphorylation; dimer; glycoprotein; growth factor receptor; phosph
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-1089/Product: platelet-derived growth factor receptor alpha #status predicted <MAT>
F;25-524/Domain: extracellular #status predicted <EXT>
F;42-102/Domain: immunoglobulin homology <IMM1>
F;143-191/Domain: immunoglobulin homology <IMM2>
F;228-292/Domain: immunoglobulin homology <IMM3>
F;428-503/Domain: immunoglobulin homology <IMM4>
F;525-548/Domain: transmembrane #status predicted <TM>
F;549-1089/Domain: intracellular #status predicted <INT>
F;591-957/Domain: protein kinase homology <KIN>
F;599-607/Region: protein kinase ATP-binding motif
F;42,76,103,179,353,359,458,468/Binding site: carbohydrate (Asn) (covalent) #status pred
F;49-100,150-189,235-290,435-501/Disulfide bonds: #status predicted
F;627/Active site: Lys #status predicted
F;849/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 40.8%; Score 2351.5; DB 1; Length 1089;
Best Local Similarity 44.0%; Pred. No. 3.5e-97;
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;

QY 8 PALAKGELL-LSLALLLPQISQGLVAVPPGPELVNVSSTFLTCGSAAPVWWRM 65
Db 6 PAFVLGCLLTGSLIUC-----QLSLPSIL-PNENKRVVVQVNSFSLKCFGESEVSQWYPM 61
QY 66 SQBPPQEM-----AKAQDGTFSVLTLTNLGLDTGEYFCTHNDSRGLTETD-ERKRLYIFV 120
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Db 62 SEESDVEIRNEENNSGLFVTVLEVSSASAHTGLYTCVYNHTQTEENELEGRHIYIV 121
QY 121 PDTVUGFLPNDABELFIFLITEITIIIPCRVTDQPLVVLHEKKGVALPVVDHQGF 180
Db 122 PDPDAVAVPLGMDYIVVEDDDSDSAIIPCRITDPTFVTLHNSEG--VVPASYSRQGF 179
QY 181 GIFEDRSYICKTIGIREVDSDAYVYVRLQVSS-INVSVNAVQTVVRQGNITLMCI 239
Db 180 GTTVGPYICATVKGKFTQIPFNVTALKATSELDLEALKTIVYKSGTIVTCAVFN 239
QY 240 NDVNVFEWTPYRKESGR--LVEFVTDFLDMFYHIRSIHLIPSAELEDSTGTYCNV 296
Db 240 NEVVLDQWYVPGVKKGITMLBEEKVPSIKLVY---TLTVPETVTKDSGDYCAAR 295
QY 297 VNDHQBEKAINITVVGSGVRLGEGVTQFABLRHSRTLOVVFEPAYPPPTVLF 356
Db 296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVGFVFEVVRAYPPPIR 355
QY 357 LGDSSAGEIALSRNVSETRYVSELTIVRVKVAEAGHYTMRAFEDAEVQLSFOLQ 416
Db 356 LIENLT-EITTDVEKIQEIRYSKLIIRAKEEDSGHYIIVAQVEDAVKSYTFELL 414
QY 417 VRVLELSSEHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS 469
Db 415 SSILDVDDHGGSTGGQTVRCGTAEGLPDIEMWICKDIKKCNNETSWTILANNV 474
QY 470 ---SEESQLENTVTVWESEQEFVSTLRLOHVDPLSVRCITLRNAVQDQTOE 526
Db 475 EIHSDRDRSTVEGRVTF-----AKVEETIAVRCLAKNLLGAENBELKL 519
QY 527 SLFPKVVVTSAILALVLTITSLIILMLWQKPRYEIRWKVIESVSSDGEHYIY 586
Db 520 TLRESEITVAANVLVILVILVILVILVILVILVILVILVILVILVILVILV 579
QY 587 LPYDSTWELPRDOLVGLRTLGSAFGQVVEATAHLSHQATMKVAVKMLKSTAR 646
Db 580 LPYDSRWEPRDGLVGLRVLGSAFGKVEGTAYGLSRSPQVMKVAVKMLKPTAR 639
QY 647 ALMSEIKIMSHLGPLHNVNLLGACTKGPIYIITEYCRYGLDVLVLRHKNHT 706
Db 640 ALMSEIKIMTHLGPLHNVNLLGACTKSGPIYIITEYCFYGLDVLVLRHNR 699
QY 707 KRPPSAELYSNAL-PVGLPLPSHVSLTGESDGYMDMSKDESVDVYVPLMD 765
Db 700 K---PKKELDIFGLNPADESTRSYVILSPENNGDYMDMKQADTTQVYV 756
QY 766 IESSNMAPVDNVYVPSAPERTCRATLINE-SPVLSYMDLVGFYSYQVANGME 824
Db 757 IQRSYDRPASVYKKKSMDSKVNLLSDNNEGLTLLDLLSFTYQVARGMEFLAS 816
QY 825 RDLAARNVLICGKLVKICDFGLARDIMRDSNVYISKGSTFLPLKMWAPESIF 884
Db 817 RDLAARNVLLAQOKIVKICDFGLARDIMHDSNVYVSGSTFLPVKMWAPESIF 876
QY 885 DVMSFGILLWEFTLGGTTPYLPPELMNEQFYNAIKRGYRMAQPAHASDEIY 944
Db 877 DVMSYGILLWEFTLGGTTPYLPPELMNEQFYNAIKRGYRMAQPAHASDEIY 936
QY 945 FEIRPPFSOLVLLERLLGEGYKKYQVDEBFLRSDHPAILRSQARLPGFH 1004
Db 937 PEKRPFSYHLSEIVENLLPQYKKYSYEKIHLDPLKSDHPAVARMR----- 984
QY 1005 SSVLYTAVQPNE-----GDNDYIILPLP--DPKPEVADSGPLEGSPSLA 1045
Db 985 DNAYIGVYTKNEEDKUKWEGGLDEORLSADSGYIILPIDIPVPEEDLGK 1044
QY 1046 S--STLNEVNTSITISCDSPLEPQDEPEPEPEPEPEPEPEPEPEPEPEPE 1103
Db 1045 SEESAETGSSSTF-----IKREDE-----TIE---DIDMDDIGIDSS 1086
QY 1104 SFL 1106
|||
```

Db 1087 SFL 1089

RESULT 5

151552

platelet-derived growth factor A receptor - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004

C;Accession: I51552

R;Jones, S.D.; Ho, L.; Smith, J.C.; Yordan, C.; Stiles, C.D.; Mercola, M.

Dev. Genet. 14, 185-193, 1993

A;Title: The xenopus platelet-derived growth factor alpha receptor: cDNA cloning and dem

ion.

A;Reference number: I51552; MUID:93365089; PMID:8358864

A;Accession: I51552

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1087 <JON>

A;Cross-references: UNIPROT:P26619; GB:M80798; NID:G214652; PIDN:AAA49929.1; PID:G214653

C;Genetics:

A;Gene: PDGFAR

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

C;Keywords: ATP; growth factor receptor

F;43-103/Domain: immunoglobulin homology <IM>

F;593-957/Domain: protein kinase homology <KIN>

F;601-609/Region: protein kinase ATP-binding motif

Query Match 40.2%; Score 2319; DB 2; Length 1087;

Best Local Similarity 44.7%; Pred. No. 9.8e-96;

Matches 505; Conservative 185; Mismatches 367; Indels 72; Gaps 21;

Qy 7 MPALAKGELLALLSLLLLEFP--ISQGLVVT--PPGPELVNVSVSTFVLTCGSAFVW 62

Db 2 MPAMRAS--LILGCLLIIGFWAILAENPLPTTFPPDKDELVQALHSSFTLKCTGSESVW 58

Qy 63 ERMSQBPQ-----MAKAQDGFSSVLTNLTLGLDTGEYFCHNDSRGLETD-ERKRL 116

Db 59 QNPNSNPEKQNVVIRSENNSGLVSVILEVSASAFDTGLTYCYHNHTQTESEIEGTDI 118

Qy 117 YIFVDPDTGVLNDAEELFITEITETPCRTVDPQLVTLHEKKGVDVALPVPYDHQ 176

Db 119 YIYVDPDNVFPAPGLFDHIIIVEEDSALVPCNTDPSSEVLKNIESRTVFAFDK 178

Qy 177 RGFSGIPEDRSYICKTTIGRDVSDAYVYRLQVS--SINVSNVAVQTVVRQGENITLMC 235

Db 179 QGFAGNPPGPGSYICETTSNMVYQTEPYILQTKATHNISVEMEA PKTFRAGETIAIDC 238

Qy 236 IVIGNDVNFWETWYPRKESRLVEPTDFLLDMPY-HIRSIILHIPSALIEDSGTYTCNV 294

Db 239 IVLNDEVVDLKWTPYQKRGVIRNVEE--SKVPYQRLVYTLTLANATTEDSGEYEC 296

Qy 295 ESNVDHDEKAINITVSVESGVRLGCVTLQPAELHRSRTLOVVFAYPPPTVLMFKDN 354

Db 297 HATLDNRVKKTWITVHEKGFIDLEPMFGSEEFANLHEVKSFVNLHAYPTPGLFMDKN 356

Qy 355 RTLDGDSAGBIALSTRNVSETRYVSELTIVRVKVAEAGHYTMRAFHDVAEVLQSLQIN 414

Db 357 RTLSENL-ETTSIVTTKETRQSKLIRAKEEDSGLYTLVAQNDRKTSYFILIQIK 415

Qy 415 VPRVLELSSHPD-SGEQTVRCRGWQPNIIWSACRLKCKCPRELPTTLGNSEEE 473

Db 416 VPALILELVDKHHGASGEQTVGCLAKMPVPDVEVLVCKDIKRCNNDTLMSIATNGSEI 475

Qy 474 SQLENTVYVEEQEPVEVSTLRLQHVDRPLSVRCTLRNAGQDTQVIVVPHSLPKV 533

Db 476 SM-----ETHQDDQ-----IESQVTFKKIETMAIRCIANLGVVAVPLKLVAPTLSEL 528

Qy 534 VISAILALVLTITSLIILMLWOKKPRYIRKWKVIESVSDGHEIYVDPMLQPLVDSTW 593

Db 529 VAAAVLVLLVILVILVILVILVILVILVILVILVILVILVILVILVILVILVILVILV 588

Qy 594 ELPRDQLVLTGRTGSGAFQGVQVETATNGLSHQATKMKVAVMLKPTARSSEKQALMSELK 653

Db 589 EFPRDGLVLRILGSGAFGKVGVEGAAYGLRSQPVMKVAVMLKPTARSSEKQALMSELK 648

Qy 654 IMSHLGPHLNVNVLGACTRGGPIYIITEYCRYGDLVDYLHKNKHTFLQHSDDKRRPESA 713

Db 649 IMTHLGAHLNVNVLGACTKSGPIYIITEYCFYGDLVNLHKNRDNFQSRHPEK--PKK 705

Qy 714 ELYSNAL-PVGLPLPHSVLTGSDGYMDKSDSDVYVPMMLDKGDKVYADIESNYM 772

Db 706 DLDIFGLNPADESTRSYVILSFENNMGDMKQADTMQYVPMLEMKPESKYSDIQRLYD 765

Qy 773 APYDNYVPSAPERTCATRLINES-PVLSYMDLVGFYSQVANGMEFLASKNCVHRDLAARN 831

Db 766 RPAS--YKKKPLSEVNILSDDDGFEGLTVLDLSFTYQVARGMEFLASKNCVHRDLAARN 823

Qy 832 VLICEGKLVIKICDFGLARDIMRDSNYISKGSTPLPKWMAPEISFNLSYTTLSDVWSFGI 891

Db 824 VLLAHGKIVKICDFGLARDIMHDSNVYKSGSTPLPKWMAPEISFDNLYTTLSDVWSFGI 883

Qy 892 LLWEITFLGTPTYPELPMNQFNNAIKRGYRMAQPAHASDEIYEIMOKCWEKEFEIRPPF 951

Db 884 LLWEIFSLGTPYPMIVDSTFNKIKSGYRMAKPDHATHEVYDVMVKCNSEPEKPSF 943

Qy 952 SQLVLLERLLGSGYKKYQVDEEFLRSDHPLRSQARLPGFHLGRSLPDTSSVLYTA 1011

Db 944 RHLSDIVESLLPMYKRCYETVLHDLKSDHPAVTR-----MRSDDNSYIGVTY 993

Qy 1012 VQPNE-----GNDNYIIPDPKPEVADEGLEGSPSLASSTLNEVNTSST 1057

Db 994 KNEHKMKDRESGDEQRLSADSGYIIPDIDPVEDE---SGKRNHSSQTSSESAIET 1050

Qy 1058 ISCDSPLEBPDEPEPPELQVPEPELEQLPDSGCPAPRAEADSFL 1106

Db 1051 GSSSSTFIKRDD-----ETIEDIDMDDDIGIDSSDL-VEDSFL 1087

RESULT 6

PFRTGA

platelet-derived growth factor receptor alpha precursor - rat

N;Contains: protein-tyrosine kinase (EC 2.7.1.112)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004

C;Accession: A34710; S33767; S25100

R;Lee, K.H.; Bowen-Pope, D.F.; Reed, R.R.

Mol. Cell. Biol. 10, 2237-2246, 1990

A;Title: Isolation and characterization of the alpha platelet-derived growth factor rece

A;Reference number: A34710; MUID:90220609; PMID:2157969

A;Accession: A34710

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1088 <LEE>

A;Cross-references: UNIPROT:P20786; GB:M63837; NID:G202929; PIDN:AAA40743.1; PID:G202930

A;Note: in the authors' translation an additional residue, Val, is shown after position

R;Herrén, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.

Biochim. Biophys. Acta 1173, 294-302, 1993

A;Title: Conservation in sequence and affinity of human and rodent PDGF ligands and rece

A;Reference number: S33764; MUID:93305723; PMID:8318539

A;Accession: S33767

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 33-149, 'R', 151-518, 'T', 520-523 <HER1>

A;Cross-references: EMBL:Z14118; NID:G56863; PIDN:CAA78488.1; PID:G56864

A;Experimental source: strain Sprague Dawley

R;Herrén, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.

submitted to the EMBL Data Library, July 1992

A;Description: Cross-species conservation in sequence and function of PDGF ligands and r

A;Reference number: S25096

A;Accession: S25100

A;Molecule type: mRNA

A;Residues: 33-149, 'R', 151-518, 'T', 520-523 <HER2>

A;Cross-references: EMBL:Z14118; NID:G56863; PIDN:CAA78488.1; PID:G56864

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

C;Keywords: ATP; autophosphorylation; glycoprotein; heterodimer; homodimer; phosphoprote

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-1088/Product: platelet-derived growth factor receptor alpha #status predicted <MAT>  
F;24-523/Domain: extracellular #status predicted <EXT>  
F;41-101/Domain: immunoglobulin homology <IMM1>  
F;142-190/Domain: immunoglobulin homology <IMM2>  
F;227-502/Domain: immunoglobulin homology <IMM3>  
F;427-502/Domain: immunoglobulin homology <IMM4>  
F;524-547/Domain: transmembrane #status predicted <TMM>  
F;548-1088/Domain: intracellular #status predicted <INT>  
F;590-956/Domain: protein kinase homology <KIN>  
F;598-606/Region: protein kinase ATP-binding motif  
F;48-99,149-188,234-289,434-500/Disulfide bonds: #status predicted  
F;75,76,88,102,178,457,467/Binding site: carbohydrate (Asn) (covalent) #status p  
F;626/Active site: Lys #status predicted  
F;848/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 40.0%; Score 2304; DB 1; Length 1088;  
Best Local Similarity 43.8%; Pred. No. 4.5e-95;  
Matches 495; Conservative 191; Mismatches 355; Indels 88; Gaps 24;

Qy 12 LKGBLLLSLLLEPOISQGLVTPPGPELVNVSTFVLTCGSGAPVWVER-MSQE-- 68  
Db 14 LTGPSLIVCQLL--PSI-----LPNENEKIVPLSSFSFLRCFGESEVSWQHPMSEED 65

Qy 69 PPOEMAKAQDGT--FSSVLTLTNLTGLDTGEYFCTHNSRGLTD-ERKRLYIFVDPDPTV 125  
Db 66 PNVEIRTEENSSLVFTVLEVNASAAHTGWYTCYNNHTQTESEIEGRHLYIYVPPDPM 125

Qy 126 GFLPNDABEELFIFLUTETETIPCRVTDQVLVTLHKKGDVALPVYDQHQRGSGIFED 185  
Db 126 AFVPLGMDTSLVIVEEDSAIIPCLTDPDTEVTLH--NNGRLVPASYSRQGFNGTFSV 183

Qy 186 RSYICKTTIGDREVDSDAYVYRLQVSS-INVSNAVQTVVROGENTILLCIVIGNDVN 244  
Db 184 GPYICEATVGRPTKSEFNVALKATSELNLEMDTRQTVYKAGETIVVTCAPVNNSEVD 243

Qy 245 FEWTYP---RKESGRVPEVPTDFLLDMPYHRSILHIPSAAELEDSGTYTCNVTESVNDHQ 301  
Db 244 LQWYTPGEVNRKNGITMLEIKLPSIKLVY---TLTPKATVKGSDGYECAAQATKEVK 299

Qy 302 DEKAINTVESGVRLGVEGTLQFAELHRSRLQVVFAYPPPTVLWFKDNRTLGDSS 361  
Db 300 EMKVTIVSVHEKGVQIRPTFGHLETVNLHQVREFVEVQAYFTPRISLWIKDNLTLIENL 359

Qy 362 AGEIATSTRNVSETRVYSELTLVRKVAEAGHYTMRAFDEAEVQLSFQIQLVNPVAVLE 421  
Db 360 T-ELTVDVRSQETRYQSKLKLRAKEEDSGHYTIIIVQDDDMKSYTFELSTLVPASILE 418

Qy 422 LSESHDPS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPELPTLLGNSSSEESQLETVN 480  
Db 419 LVDDHSGSGGQTVRCCTAEGTFLPNIEMWICKDIKKCNNDTSWTVLA-----SNVSNII 472

Qy 481 TYWEEEEQFEVWSTRLQHVDRPLSVRCTLNVAVGQDTQEVIVPHSLPFAVWVISAIA 540  
Db 473 TEPHQRGSTVEGRVSPFAKVEETIAVRLAKNDLIGNRELKLVAPSRSELTVAIAAVLV 532

Qy 541 LVLVTISLILMLWOKPRYEIRWKVIESVSDGHEIYVDDMQLPYDSTWELPRDQL 600  
Db 533 LLVIVIVSLIVLVINWQKPRYELRWVIESISPDGHEIYVDDMQLPYDSRWEFFRDGL 592

Qy 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVQMLKSTARSSEKQALMSKIMSHLGP 660  
Db 593 VLGRITLGSAGFGKVEGTAYGLSRSPVMKAVVQMLKPTARSSEKQALMSKIMTHLGP 652

Qy 661 HLNVNLLGACTGGPIYIITEYCRYGDLVDYLHRNKHFTLOHSDKRRPSPSAELYSNAL 720  
Db 653 HLNIVNLLGACTSGPIYIITEYCRYGDLVDYLHRNKHRSFMSRHPK---PKDLDIFGL 709

Qy 721 -PVGLPSPHVSITGESDGGVMDMSKDESVDYVPMIDMKGDVKYADTESNNYMAPYDNYV 779  
Db 710 NPADESTRSVILSFENNNGDYVDMKQADTQYVPMLEKREKSKYSDIQRSLYDRPASYKK 769

Qy 780 PSAPERTCRATLI-NESFVLISMDLVGFSYQVANGMEFLASKKNCVHRDLAARNVLIPEGK 838

770 KSMLESEAKNLLSDDDSEGLTLLDLLSFTYQVARGMEFLASKKNCVHRDLAARNVLLAQGK 829  
Qy 839 LVKICDFGLARDIMRDSNYISKSGSTFLPKWMAPEISFNSLYTTLSDVWSFGILLWEIFT 898  
Db 830 IVKICDFGLARDIMRDSNYISKSGSTFLPKWMAPEISFIDNLYTTLSDVWSYGVLLWEIFS 889  
Qy 899 LGCTPPPELPMNOFYNAIKRGYMAQPAHASDIIEIMOKCWEEKFEIRPPFPFSQVLVLL 958  
Db 890 LGCTPPPGMWDSTFFYNKIKSGYMAKPDHATSEVIEIMVQCWNSEBEKEPSPFHLSEIV 949  
Qy 959 ERLLEGYKKYQVDEEFRLSRDHPAILRSQARLPQGHGRLSPDTSVLYTAVQVNE-- 1016  
Db 950 ENLLPGYKKSYEKIHLDFLKSHPAVARNR-----VDSNAYIGVTYKNEED 997

Qy 1017 -----GNDVIIILP--DPKPEVADEGLEGSPSLAS--STLNEVNTSST 1057  
Db 998 KLKEWEGGLDEQLSADSGYIILPDIQVPEEDLGKRNHSSQTSSEAIETGSSSST 1057

Qy 1058 ISCDSPLEPODEPEPEPQLQVEPEPELQLPDSCPCAPRAEAEDSFL 1106  
Db 1058 F-----IKREDE-----TIE---DIDMDDIGIDSSDL-VEDSFL 1088

RESULT 7  
S33727  
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: I57511; S33727  
R;Stiles, C.D.; Wang, C.  
Mol. Cell. Biol. 10, 6781-6784, 1990  
A;Title: Retinoic acid promotes transcription of the platelet-derived growth factor alpha  
A;Reference number: I57511; MUID:91061789; PMID:2174116  
A;Accession: I57511  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1089 <RES>  
A;Cross-references: UNIPROT:P26618; GB:M57683; NID:g199783; PIDN:AAA39733.1; PID:g199784  
C;Genetics:  
A;Gene: PDGF-alpha-R  
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
C;Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transmembrane  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;228-292/Domain: immunoglobulin homology <IMM>  
F;591-957/Domain: protein kinase homology <KIN>  
F;599-607/Region: protein kinase ATP-binding motif  
F;42,76,89,103,179,353,359,458,468,506/Binding site: carbohydrate (Asn) (covalent) #status p

Query Match 39.4%; Score 2271.5; DB 1; Length 1089;  
Best Local Similarity 43.8%; Pred. No. 1.3e-93;  
Matches 494; Conservative 185; Mismatches 365; Indels 83; Gaps 23;

Qy 17 LLSLLLLLELPQISQGLV---VTPPGPELVNVSTFVLTCGSGAPVWVER-MSQE--PP 70  
Db 9 LVLSCLLTGRLISQCLLLPSILPNEKIVQLNSSFSLRCVGESEVSWQHPMSEEDPN 68

Qy 71 QEMAKAQD--GTSSVLTTLNLTGLDTGEYFCTHNSRGLTD-ERKRLYIFVDPDPTVGF 127  
Db 69 VEIRSENNNSGLVTVLEVVNNSAAHTGWYTCYNNHTQTDSEIEGRHLYIYVPPDPMF 128

Qy 128 LPNDABEELFIFLUTEITIPCRVTDQVLVTLHKKGDVALPVYDQHQRGSGIFEDRS 187  
Db 129 VFLGMDTSLVIVEEDSAIIPCTTPTQVTLH--NNGRLVPASYSRQGFNGTFSVGP 186

Qy 188 YICKTTIGDREVDSDAYVYRLQVSS-INVSNAVQTVVROGENTILMCIVIGNDVNFE 246  
Db 187 YICEAAVKGRFTKTSFNFVYALKATSELNLEMDARQTVYKAGETIVVTCAPVNNVVDLQ 246

Qy 247 WTPY---RKESGRVPEVPTDFLLDMPYHRSILHIPSAAELEDSGTYTCNVTESVNDHQ 303  
Db 247 WTPYGGVRNKGITMLEIKLPSIKLVY---TLTVPRATVKGSDGYECAAQATKEVK 302

QY 304 KAINITVVSQYVLLGEVGTLPFAELHRSTLTQVPEAYPPPTVLWPKNRTLTGSSAG 363

DB 303 KRVITISHEKGFYEIPTFSQLEPVLNHEVREFVVEVQAYPTPRISWLKNLTLENLT- 361

QY 364 EIALSTRNVSETRYVSELTLVRVKAAGHYTMAFHEDAEVQLSQFQIQINVPVRLS 423

DB 362 EITTDVQSQETRYQSKLKLIRAKEEDSGHYTIIQNEDDVKSYTFELSTLVPASILDV 421

QY 424 ESHPOS-GEQTVRCRGRGMPQPMNIISACRDLKRCPRBLPPTLLGNSEBESOLETNVY 482

DB 422 DDHGGGGGQTVRCTABEGLPEIDMCKIKKCNNDTSWTLA-----SNVSNIIIE 475

QY 483 WEEBQEFVSTLRLOHVDPLSRVCTLRNAVGDQTEVIVVPHSLPKVWVVISAILAV 542

DB 476 LPRRGSTVEGRVSFAKVEETIAVCLAKNLSVVARELKLVAPTLRSELTVAEAVLVLL 535

QY 543 VLTITSLIILIMLWQKPRYEIRWKVIESVSSDGHEYIYVDPMLPYDSTWELPRDQVL 602

DB 536 VIVIVSLIVLWIKQPRYEIRWRVIESIPDGHEYIYVDPMLPYDUSRWEFPRDGLVL 595

QY 603 GRTLSGAFQGVVEATAHGLSHSQATMKVAKMLKSTARSEKQALMSSELKIMSHLGPL 662

DB 596 GRILSGAFQGVVEGTAYGLSRSPQVMKVAVKMLKPTARSEKQALMSSELKIMTHLGPL 655

QY 663 NVNLLGACTKGPIYIITEYCRYGDLVDYLHRNKHFTLOHSDKRPSPSABLYSNAL-P 721

DB 656 NIVNLLGACTKSGPIYIITEYCFYGDVLVNYLHKNRDSFMSQHPEK---PKKOLDIFGLNP 712

QY 722 VGLPLPSHSLTGESDGVGMDMSKDESDVYVPMMDKMGDKVYADIESNTYMAPYDNYVPS 781

DB 713 ADESTRSYVILSPENNNGDYMDKQDDTTQYVPMLEKVEYSYDIQRLYDRPASYYKKS 772

QY 782 APERTCRATLI-NESPVLSYMDLVFGSYQVANGMEFLASKNCVHRDLAARNVLI CEGKLAV 840

DB 773 MLDSEVKNLSDDDSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIV 832

QY 841 KICDFGLARDIMRDSNVISKSGTFLPLKMWAPESIFNSLYTTLSDVMSFGILLWEIFTLG 900

DB 833 KICDFGLARDIMHDSNDVSKSGTFLPLKMWAPESIFNLNLYTTLSDVMSYGILLWEIFSLG 892

QY 901 GTPYPPLMNEQFYNAIKCRYRMAQPAHASDEIYEIMQKWEKEFEIRPPFSQVLLLER 960

DB 893 GTPYPGMVDSTFYNKIKSGYRMAKPHATSEVYEIMVQCWNSDPEKRPFSYHLSEILEN 952

QY 961 LLGEGYKKYQVDEEFLRSDHPAILRSQARLPGFHGLRSLDTSVLYTAVQPN-----1016

DB 953 LLPGYKKYKYEKHLDFLKSDFHFAVRM-----VDSNAYIGTYKNEEDKL 1000

QY 1017 -----GNDNYIITLP--DPKPEVADEGLEGPSLAS--STLNEVNTSSTIS 1059

DB 1001 KDWEGLDEQRLSADSGYIITLPDIDVPVEEDLGKRNHSSQTSESAIETGSSSTF- 1059

QY 1060 CDSPLPEQPEPEPQLEQVPEPELEQLPDSGCPAPRAEADSFL 1106

DB 1060 -----IKREDE-----TIE---DIDMMDDIGIDSDL-VEDSFL 1089

RESULT 8

S33766

platelet-derived growth factor receptor beta - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 03-Mar-1994 #sequence\_revision 12-Apr-1996 #text\_change 09-Jul-2004

C:Accession: S33766; S25098

R:Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.

Biochim. Biophys. Acta 1173, 294-302, 1993

A:Title: Conservation in sequence and affinity of human and rodent PDGF ligands and receptors

A:Reference number: S33764; MUID:93305723; PMID:8318539

A:Accession: S33766

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-499 <HER1>

A:Cross-references: UNIPROT:Q05030; EMBL:Z14119; NID:G56869; PIDN:CAA78489.1; PTD:G56870

A:Note: the sequence of residues 497-499 is not given in this paper







Db 334 DLVVEFEAYPKPHQOHWYMNRT--PTNRGDEYVKSNDQSNIRYVNELRILRLKGTGGT 391  
Qy 394 YTMRAFHEDAEOVLSFOLOLNVPVRLVLESGESHPDSGEQTVRCRGRGMPQNIWISACRD 453  
Db 392 YTFVNSDVSAVTFDVTYNTPEIL-----TYDRLMNGRLQCVAGFPPTDWFCTG 447  
Qy 454 L-KRCPRELPPT-----LLGNSSEESQLETNVTYVEEEOEFVSTLRLQ 498  
Db 448 AEQRCTVPVPPVDQIQNASVSPFGKLWQSSIDSSVFRHNGT----- 490  
Qy 499 HVDRPLSVRCLTNAVQODT-----QEVIVPHSLPFPKVVISAILALVLTIIIS 548  
Db 491 -----VECKASNAVGKSAFFNAFPAKNGSKQIQPHTL-FTPELLGFVVTAGLMGII- 541  
Qy 549 LIILIMLWOKPPEYERKWKVIESVSSDGHEIYVDPMPOLPYDSTWELPRDLVGRITGS 608  
Db 542 VMVLAKYKLOKPMVEQWKVVEI--NGNNYVIDPTQLPYDHKWEPFRNLSFGKITLGA 599  
Qy 609 GAFQGVVEATAHGLSHSQATMKVAVKMLKSTARSSKQALMSSELKIMSHLPHLNVNLL 668  
Db 600 GAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSLKVLSYLGNNHNIWNLL 659  
Qy 669 GACTKGPIIITIEYCHRYGDLVYLHRNKHTFLOHSDKRRPPSAEILSYNALPVGLPLPS 728  
Db 660 GACTVGGPTLVITIEYCYGDLNLFRLKRKDSFI--FSKQEOQADAALYKNLL----- 709  
Qy 729 HVSLTGSDGYMDMSKDESVDVPMPLDMKGVKY-----ADIESNYMAPYDNYVPSAP 783  
Db 710 HSK-----ESSCDSNEY---MDMKPGVSYVPTKTDRS---ARISYI----- 749  
Qy 784 ERTCRATLINESPV-LSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGLVKI 842  
Db 750 ERDVTAPMEDDELALDLELLSFSYQVAKGMFLASKNCIHRDLAARNILLTHGRITKI 809  
Qy 843 CDFGLARDIMRDSNYISKSGTFPLKWMAPESIFNSLYTTLSDVSWSGILLWEIFLTGGT 902  
Db 810 CDFGLARDIRDSNYVYKNGARLPFKWMAPESIFNCVYTFESDVSWSYGIFELWELFSGSS 869  
Qy 903 PYPELPMNEQFYNAIKRGYMAOPAHASDIYEIMQCKWEKFEIRPPFQOLVLLERLL 962  
Db 870 PYGMPVDSFYKMKIEGFRMLSPHAPAAVEVMKTCNDADPLKRTFFQVQLIEKQI 929  
Qy 963 GEGYKKYQOVBEEFLRSDPAILRSQARL 992  
Db 930 SDSSKHIYSLNLCNPNPNPVVDHSHVRV 959

RESULT 11  
TMVMD  
protein-tyrosine kinase (EC 2.7.1.112) fms precursor - feline sarcoma virus (strain McDr  
C;Species: feline sarcoma virus  
A;Note: host Felis sp. (cat)  
C;Date: 27-Nov-1995 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C;Accession: A00654  
R;Hampe, A.; Gobet, M.; Sherr, C.J.; Galibert, F.  
Proc. Natl. Acad. Sci. U.S.A. 81, 85-89, 1984  
A;Title: Nucleotide sequence of the feline retroviral oncogene v-fms shows unexpected ho  
A;Reference number: A00654; MUID:84119469; PMID:6582485  
A;Accession: A00654  
A;Molecule type: DNA  
A;Residues: 1-941 <HAM>  
A;Cross-references: UNIPROT:P00545  
C;Comment: This protein is synthesized as a gag-fms polyprotein.  
C;Genetics:  
A;Gene: fms  
A;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;  
otein kinase  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-941/Product: protein-tyrosine kinase fms #status predicted <MAT>  
F;24-509/Domain: extracellular #status predicted <EXT>  
F;35-86/Domain: immunoglobulin homology <IMM1>  
F;120-179/Domain: immunoglobulin homology <IMM2>

F;217-280/Domain: immunoglobulin homology <IMM3>  
F;316-381/Domain: immunoglobulin homology <IMM4>  
F;410-484/Domain: immunoglobulin homology <IMM5>  
F;510-534/Domain: transmembrane #status predicted <TM>  
F;535-941/Domain: intracellular #status predicted <INT>  
F;577-915/Domain: protein kinase homology <KIN>  
F;585-593/Region: protein kinase ATP-binding motif  
F;42-84,127-177,224-278,417-482/Bisulfide bonds: #status predicted  
F;45,73,94,153,275,286,302,335,410,477,490/Binding site: carbohydrate (Asn) (covalent) #  
F;613 630,776/Active site: Lys, Glu, Asp #status predicted  
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 24.7%; Score 1421.5; DB 1; Length 941;  
Best Local Similarity 35.5%; Pred. No. 5.8e-56;  
Matches 371; Conservative 155; Mismatches 347; Indels 171; Gaps 36;

Qy 19 LSLILLLEPOISQGL-VMTPPGPELVNVSSTFLVTCSGSAPVWE-----RMSDEPP 70  
Db 6 LLVLLMATAWHAQGVPIQSPGPELVVEPGTTVTLRCVNGSVEMDGPISPHNLDLDPP 65  
Qy 71 QEMAKAQDGTFFSSVLTLTNLTLGDTGEYFCTH--NDSRGLTDERKRLYIFVDPDPTVGFL 128  
Db 66 -----SSILTNNTATFQNTCTYHCTEPNPRGNAT-----IHLVYKDP----- 104  
Qy 129 PNDAELFLFLTEIT-----EITPCRVTDPLV--VTLHEKKGDVAL---PVPYDHQRG 178  
Db 105 ---ARPKVLAQEVTVLEQDALLPCLLTDPALAEAGVSLVRVGRPVLRTQNTYSFSPWHG 161  
Qy 179 F----SGIEDRSYICKTIGDREVDSDAYV-YRLQVSS-INVSVNAVTVVRQGENIT 232  
Db 162 FTIHKAKFIENHVYQCSARVDGRTVTSMGLWLVKQKDISGPATLTILEPABLVIQGBAAQ 221  
Qy 233 LMCIVIGNDVNPWEVTPRKESGRVPEVPTDFLLDMPYHIRSIHLHPSAELEDSGYTCN 292  
Db 222 IVCSASNID-VNFDVSLRHCDTKLTISQQSDF-HDNRVQKVLTLNLDHVSFDQAGNYSCT 279  
Qy 293 VTESVNDHDEKAINITVVEGVYVRLGEGVTGTOFAPAEHLRSRTLOVVFAYPP-PTVLWF 351  
Db 280 ATNAGNH--SASMVPRVVEASVSNLTSEQLLQEVTVGKEVLDQVKVEAPGLESFNW- 336  
Qy 352 KDNRTIGDSAGEIALSTRNVSET-RVVSLETLVRVKVAEAGHYTMRAFHEDEAVQLSFQ 410  
Db 337 ---TYLGPFSYQDKLDFVTIKDYTTSTLSPLRKRSESGYSYFLARNAGQNALTFE 393  
Qy 411 LQINVP--VRV-LELSSEHPDSGEQTVRCRGRGMPQNIWISACRD-LKRCPRELPPTLL 466  
Db 394 LTLRYPEVRVTMLI-----NGSDILLCEASGPQSPSVTVVQCRSHDTCDESAGLVLE 448  
Qy 467 GNSSEESQLETNVTYVEEEOEFV--STLRLOHVDRLPLSVRCTLNNAVQDQTOEV--- 521  
Db 449 DSHSEVLQVPP-----YEVIVHSLLAITGLEHNRNRYECRAFNSVGNSSQTFWPI 498  
Qy 522 -----IVVPHSLPFKVVVISAILALVLTIIISILIMLWOKPPEYERKWKVIESVSDG 576  
Db 499 SIGAHTPLPDELLFTPTVLLTC-MSIMALLLLLLLLLLLYKQKPKYQVRWKILIESY--EG 555  
Qy 577 HEYIYVDPMPOLPYDSTWELPRDLVGRITGSAGFQVVEATAGHLSHQAATMKVAVKML 636  
Db 556 NSYTFIDPTQLPNEKWEPRNNLQFGKTLGTGAFGKVVEATAFGLKEDAVLKVAVKML 615  
Qy 637 KSTARSEKQALMSSELKIMSHLPHLNVNLLGACTKGGPIYIITEYCRVGDLDVYLHRN 696  
Db 616 KSTAHADKEALMSSELKIMSHLQHENIVNLLGACTHGGPVLVITTEYCCYGDLLNLFUR- 674  
Qy 697 KHTFLQHSKRRPPSAEILSYNALPVGLPLPS-HVSLTGSDGYMDMSKDESVDVYVPM 755  
Db 675 -----QAE-----AMPGPSVSGQDPEAGAGYKNHLEK----- 703  
Qy 756 DMKGDVKYADIESNTMAPYDNTVPSAPERTCRATLINES-----PVLSYMDLV 804  
Db 704 -----KYVRDSDGFSQGVDTIVEMRPVSTSS---NDSFSEEDLKEDGRPLELRDL 754  
Qy 805 GFSYQVANGMEFLASKNCVHRDLAARNVLICEGLVKICDFGLARDIMRDSNYISKSTP 864

Db	755	HFSSQVAGQMAFLASKNCIHRDVAARNVLLTSGRVAKIGDGFGLARDIMNDSNIYIKGNAR	814
Qy	865	LPLKWMAPESIFNSLYTTLSDVWSFGILLWEFTLTGGTPYPYELPNWNEQFYNAIKGYRNA	924
Db	815	LPVKWMADESIFDCVYTVQSDVWSYGILLWEFLSGLNPYGPILVNSKPYKLVKQGYQNA	874
Qy	925	QPAHASDRIYIMQKWBKEFIRPPFSQVLVLLRLGLGEGYKKYQQVDEFLRSDHPA	984
Db	875	QPAFAPKNYISIMQACWALEPRTTRFTQICSLQK-----QAQED-----	915
Qy	985	ILRSQARLPGFHGLRSLDTSVL	1008
Db	916	-----RRVPNTNL--PSSSSRL-932	
RESULT 12			
JN0677			
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - chicken			
N;Alternate names: tyrosine kinase receptor kit			
C;Species: Gallus gallus (Chicken)			
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004			
C;Accession: JN0677			
R;Sasaki, E.; Okamura, H.; Chikamune, T.; Kanai, Y.; Watanabe, M.; Naito, M.;			
Gene 128, 257-261, 1993			
A;Title: Cloning and expression of the chicken c-kit proto-oncogene.			
A;Reference number: JN0677; MUID:93292995; PMID:7685729			
A;Accession: JN0677			
A;Molecule type: mRNA			
A;Residues: 1-960 <SAS>			
A;Cross-references: UNIPROT:Q08156; DDBJ:D13225; NID:g303532; PIDN:BAA02506.1;			
A;Experimental source: brain			
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin			
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming			
rotein kinase			
F;1-24/Domain: signal sequence #status predicted <SIG>			
F;25-960/Product: tyrosine kinase receptor #status predicted <MAT>			
F;314-380/Domain: immunoglobulin homology <IMW>			
F;573-916/Domain: protein kinase homology <KIN>			
F;581-589/Region: protein kinase ATP-binding motif			
F;76,135,149,269,286,306,318,338,356,453,469/Binding site: carbohydrate (Asn)			
Query Match 24.3%; Score 1401.5; DB 1; Length 960;			
Best Local Similarity 34.9%; Pred. No. 4.6e-55;			
Matches 352; Conservative 161; Mismatches 368; Indels 127; Gaps 32			
Qy	3	LPGAMPALAKGELLISLLLLLPEQISQGLVVTTPGPELVLVNSSTFVLTCSGAPVW	62
Db	1	MEGAHLAWELAHAVLLLSL-----IPAGSVPHRESSLVNKGELRLCKNEEGPTW	53
Qy	63	ERMSEPPQEMAKAQDGTFSSVLTLNLTGDTGYFCTHDSRGLETDERKRLYIFVPD	122
Db	54	NFQNSDPSAKTRISNEKEWHT---KNATIRDIGYEC---KSKGSIVNS---FVYVKD	103
Qy	123	PTVCFPLNDABELIFLTFEITPCVTPDQV-VTLHEKKGDAVLPVYDH-----	175
Db	104	PNVLFLVDS-----LIYGKEDSDILLVCPLTDPVLFNLTFRKCDGK--PLPKNMTFIPNP	156
Qy	176	-----QRFGSGIFEDRGVICTTIGDREVDSDAYVYRLQVSSIN-----VSVNAV	221
Db	157	QKGIIIKNVQSRFGCYQ-----CLAKNGVEKISEHIF--LNVRPVHKALPVLTLSK	208
Qy	222	QTVVRQENITLMCIVIGND-VNPEWTYPKESGRVPEVPTDFLLDMPYHRSITLHIPS	280
Db	209	YELKEGEFEFTVCITTDVDSVSKASWI---SYKSAIVTSKRNLDGYERKFLTNIRS	265
Qy	281	AELSDSGYTCNVTVESVNDHODEKAINITVYESGVYRLLGVLGTQLQFAELHRSRTLQVVF	340
Db	266	VGVNDSEFTQAEHPFG--KTNATVTLKALAKGFVRLFATNTTIDINAGQNGLTVEY	323
Qy	341	EAYP-PPTVLWFKNRTLGDSSAGEIALSTRNVSTRVYSELTLVRVKVAEAGHYTMRAF	399
Db	324	EAYPKPEEVMWYNETLQNSDHYVKEFT--VGNNSYTSSELHTRLKGTEGIGYTFVFS	381

A>Note: sequence extracted from NCBI backbone (NCBIN:78839, NCBI:78842)  
A>Note: disease-related mutant from patient with piebaldism  
A:Accession: B41815  
A:Molecule type: DNA  
A:Residues: 637-641, 'SPBLPW' <SP2>  
A:Cross-references: GB:S78843; NID:g244086; PIDN:AAB21235.1; PID:g244087  
A>Note: sequence extracted from NCBI backbone (NCBIN:78843, NCBI:78844)  
A>Note: disease-related mutant from patient with piebaldism  
A:Accession: C41815  
A:Molecule type: DNA  
A:Residues: 556-560, 'GGDKWK' <SP3>  
A:Cross-references: NID:g244088; PIDN:AAB21236.1; PID:g244089  
A>Note: sequence extracted from NCBI backbone (NCBIN:78845, NCBI:78846)  
A>Note: disease-related mutant from patient with piebaldism  
R:Giebel, L.B.; Strunk, K.M.; Holmes, S.A.; Spritz, R.A.  
Oncogene 7, 2207-2217, 1992  
A:Title: Organization and nucleotide sequence of the human KIT (mast/stem cell growth factor receptor) gene  
A:Reference number: 137948; MUID:93064697; PMID:1279499  
A:Accession: 137948  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-976 <RES>  
A:Cross-references: EMBL:X69301; NID:g34089; PIDN:CAA49159.1; PID:g825686  
A>Note: an alternative splice form omitting residues 510-513 is described  
R:Yamamoto, K.; Tojo, A.; Aoki, N.; Shibuya, M.  
Jpn. J. Cancer Res. 84, 1136-1144, 1993  
A:Title: Characterization of the promoter region of the human c-kit proto-oncogene.  
A:Reference number: 156954; MUID:94103107; PMID:7506248  
A:Accession: 156954  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-22 <RE2>  
A:Cross-references: GB:S67773; NID:g459358; PIDN:AAB29529.1; PID:g459359  
R:Spritz, R.A.; Holmes, S.A.; Berg, S.Z.; Nordlund, J.J.; Fukui, K.  
Hum. Mol. Genet. 2, 1499-1500, 1993  
A:Title: A recurrent deletion in the KIT (mast/stem cell growth factor receptor) proto-oncogene  
A:Reference number: 154336; MUID:94061059; PMID:7694728  
A:Accession: 154336  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 242-250 <RE3>  
A:Cross-references: GB:S67686; NID:g460545; PIDN:AAD13996.1; PID:g4261696  
C:Genes: GDB:KIT  
A:Cross-references: GDB:120117; OMIM:164920  
A:Map position: 4q12-q12  
A:Introns: 23/1; 113/1; 207/1; 252/3; 309/1; 372/2; 411/1; 449/2; 514/1; 549/3; 592/1; 641/1  
A>Note: defects in this gene may result in piebaldism  
C:Function:  
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP  
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;  
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; kinase-related  
protein; tyrosine-specific protein kinase  
F:1-976/Product: protein-tyrosine kinase  
F:1-509,514-976/Product: protein-tyrosine kinase kit precursor, long form #status predicted <NAT>  
F:1-22/Dominant: signal sequence #status predicted <SIG>  
F:23-976/Product: protein-tyrosine kinase kit #status predicted <NAT>  
F:23-520/Dominant: extracellular #status predicted <EXT>  
F:51-99/Dominant: immunoglobulin homology <IMM1>  
F:129-188/Dominant: immunoglobulin homology <IMM2>  
F:226-292/Dominant: immunoglobulin homology <IMM3>  
F:328-394/Dominant: immunoglobulin homology <IMM4>  
F:423-493/Dominant: immunoglobulin homology <IMM5>  
F:521-543/Dominant: transmembrane #status predicted <TMW>  
F:544-976/Dominant: intracellular #status predicted <INT>  
F:587-931/Dominant: protein kinase #status predicted <KIN>  
F:595-603/Region: protein kinase ATP-binding motif  
F:58-97,136-186,233-290,428-491/disulfide bonds: #status predicted  
F:130,145,283,293,300,320,352,367,463,486/Binding site: carbohydrate (Asn) (covalent) #s  
F:623,640,792/Active site: Lys, Glu, Asp #status predicted  
F:797,810/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 24.3% Score 1400.5; DB 1; Length 976;

Best Local Similarity 35.1%; Pred. No. 5.2e-55;  
Matches 360; Conservative 159; Mismatches 339; Indels 169; Gaps 36;  
QY 18 LLSLLLLL-----EPOISQGLAVTP-----PG-PELVANVSSTFVLTCGSAFVPMV--- 62  
DB 11 LCVLLLLLVQSGSQSPVSPGEPSPSPHPOKSDLVIVRGDEIRLLCTDTPGPKVTFEI 70  
QY 63 -----ERMSQEPPEQMAKAQDGTFFSVLTLTNLTGLDGTGYFCTHNDSGRLGLETDERKRLY 117  
DB 71 LDETNENKQNEWITEKAEA-----TN-----TGKTYTCT--NKHGLSNS-----IY 108  
QY 118 IFVPPPTVGFLENDAEELFIFLITEITIPCRVTPDQLVTLHEKKGDAVALPVVPY---- 173  
DB 109 VFVRDPAPKFLVDRS-----LYGKEDNDTLVRCPFLDPE--VTNYSUKGCGKPLPKDLRF 162  
QY 174 --DHORGFGSIPEDRSY--ICKTTIGDREVDSDAYVYVRLQVSSI-----NVSNNAVQTV 224  
DB 163 IFDPKAGIMIKSVKAYHRLCLHCSVDQSGKSVLSEKFIKVRPAKFAVNVSVSKASYL 222  
QY 225 VROGENITLMCIVIGNDVVNFVTPYRKESG--RLVEPVTDLL--DMPYHIRSLHIPSA 281  
DB 223 LREGGEFTVTCI--KDVSSSVYSTWKRENSQTKLQEKYNSWHHGGDFNYERQATLTISSA 280  
QY 282 ELEDSTGYTCNVTSVNDHQDEKAINIT-----VWESGYVRLGGEVCTLOFAELHRSRTLQ 337  
DB 281 RVNDSGVFCYANNTFG-----SANVTTTLEVDKGFNIPFMINTTVFVNDGENVDLI 334  
QY 338 VYFEAYPPPT-VLWFKDNRNLGDSAGETALSTRNVSETRYVYSELTLVRVKVAAEAGHYTM 396  
DB 335 VYEYAFPRPEHOOMIYMNRTFTDK--WEDYPKSESNIRYVSELHLTLKGTGEGTYTF 392  
QY 397 RAFHEDAEVQLSFQLOINPVVRVLELSESHPSDGEQTVRCRCRGMPPQNIIMSACRDL-K 455  
DB 393 LVNSNDVNAIAAFNVVNTKPEIL-----TYDRLVNGMLQVAAAGPPEPTIDWYFCPQTEQ 448  
QY 456 RCPRELPT-----LLGNSSEESQLENTVNTYVEEESQEFVWSTLRLQHVD 501  
DB 449 RCSASVLPVDVQTLNSSGPPFKLVQSSIDSAPFKHNGT----- 488  
QY 502 RPLSVRCLRNNAVGDOT-----QEVIVVPHSLPFKVVVISAILALVLTITSLII 551  
DB 489 -----VECKAYNDVGKTSAYFNFAFKNNKEQIHPHTL--FTPLLIGFVIVAGMCI--VMI 542  
QY 552 LIMLMQKPRYRIRKWKVIESVSSDGHETIYVDPMLQPYDSTWELPRDQLVLGRTLSGAF 611  
DB 543 LTYKYLQKPMYEQWKVBEI--NGNNVYVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAF 600  
QY 612 QGVTEATAHLSHQNTMKVAVKMLKSTARSSEKQALMSELKIMSHLGPLHNVNLLGAC 671  
DB 601 GKVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVLKSLGNHNMIVNLLGAC 660  
QY 672 TKGGGYIITEYCRYGDLVDYLHRNKHFTL-----QHSKRRRPPSAEYLSNALPVGLPLP 727  
DB 661 TIGGPTLVITECCVGDLLNLFRRKDSFICKQEDHAE-----AALYKYL-----LH 708  
QY 728 SHVLTGSDGGYMDMSKDESVDYVPMPLDMKGVADYDISSNYMAPYDNYVPSAPERTC 787  
DB 709 SKESSCSDSTNEYDMK--PGVSIV--VPTKAD-KRRSVRIGSYI-----ERDV 752  
QY 788 RATLINESPV-LSYMDLVGFSQVANGMEFLASKNCVHDLAARNVLCCEGLVKLCDFG 846  
DB 753 TPAIMEDDEDLAULDELLSFSYQVAKGMAFLASKNCIHRDLAARNLTLLTHGRITKICDFG 812  
QY 847 LARDIMRDSNYISKSTFPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLGGTTPYE 906  
DB 813 LARDIKNDSNVYVKNARLPVKWAPESIFNCVTFESDVWSVIGIFLWELFSLGSSPYPG 872  
QY 907 LPMNEQFYNAIKRGYRMAQAPAHASDIYIMQKWEKEFEIRPPFSQVLVLLBRLGEGY 966  
DB 873 MPVDSKFYKWKKEGFRMLSPHAPAEYDIKMTCDADPLKRPFTKQIVQLIEKQISEST 932  
QY 967 KKKYQOV 973





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2005, 05:13:43 ; Search time 144.611 Seconds  
(without alignments)  
3916.424 Million cell updates/sec

Title: US-10-027-400-4  
Perfect score: 5766  
Sequence: 1 MRLPGAMPALKLGELLLS.....EQLPDSCGPAPRAEADSEFL 1106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5762	99.9	1106	1 PGDR HUMAN	P09619 homo sapien
2	5206.5	90.3	1103	2 O6QNF3	O6qnf3 canis famil
3	4976.5	86.3	1097	1 PGDR RAT	Q05030 rattus norv
4	4972	86.2	1098	1 PGDR MOUSE	P05622 mus musculu
5	4957.5	86.0	1099	2 Q7TMR8	Q7tmr8 mus musculu
6	2403	41.7	1048	2 P79749	P79749 fugu rubrip
7	2351.5	40.8	1089	1 PGDS HUMAN	P16234 homo sapien
8	2319	40.2	1087	1 PGDS XENLA	P26619 xenopus lae
9	2317	40.2	1087	2 Q7ZV71	Q7zv71 xenopus lae
10	2304	40.0	1088	1 PGDS RAT	P20786 rattus norv
11	2303	39.9	1079	2 Q6E7G6	Q6e7g6 canis famil
12	2292.5	39.8	1089	1 PGDS MOUSE	P26618 mus musculu
13	2292.5	39.8	1089	2 Q7TSJ3	Q7tsj3 mus musculu
14	2270	39.4	1087	2 Q9PUF6	Q9puf6 gallus gall
15	2210	38.3	1059	2 Q9D849	Q9de49 brachydanio
16	2175.5	37.7	1082	2 Q8AXC7	Q8axc7 fugu rubrip
17	2142.5	37.2	1078	2 Q8AXC8	Q8axc8 fugu rubrip
18	2085	36.2	986	2 Q8UVR9	Q8uvr9 fugu rubrip
19	1538.5	26.7	790	2 Q8CAN3	Q8can3 mus musculu
20	1531	26.6	686	2 Q75WK5	Q75wk5 oryzias lat
21	1496	25.9	743	2 Q6PAH5	Q6pah5 homo sapien
22	1445	25.1	976	2 Q8JFR5	Q8jfr5 brachydanio
23	1445	25.1	976	2 Q9W755	Q9w755 brachydanio
24	1432.5	24.8	980	1 KFM5 FELCA	P13369 felis silve
25	1426	24.7	974	2 Q63702	Q63702 rattus norv
26	1425	24.7	978	2 Q63116	Q63116 rattus norv
27	1424	24.7	978	1 KFM5 FSWMD	P00545 feline sarc
28	1404.5	24.4	972	2 Q761I0	Q76i10 callithrix
29	1404	24.3	975	1 KIT CANFA	Q97799 canis famil
30	1404	24.3	975	2 Q7YRV7	Q7yrv7 canis famil
31	1403	24.3	979	2 Q8WN23	Q8wn23 canis famil

## RESULT 1

ID	PGDR HUMAN	STANDARD;	PRT;	1106 AA.
AC	P09619; Q8NSL4;			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	Beta platelet-derived growth factor precursor (EC 2.7.1.112)			
DE	(PDGF-R-beta) (CD140b antigen).			
GN	Name=PDGFRB;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88217915; PubMed=2835772;			
RA	Gronwald R.G.K., Grant F.J., Haldeman B.A., Hart C.E., O'Hara P.J.,			
RA	Hagen F.S., Ross R., Bowen-Pope D.F., Murray M.J.;			
RT	"Cloning and expression of a cDNA coding for the human platelet-			
RT	derived growth factor receptor: evidence for more than one receptor			
RT	class.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:3435-3439(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89096941; PubMed=2850496;			
RA	Claesson-Welsh L., Eriksson A., Moren A., Severinsson L., Ek B.,			
RA	Oestman A., Besholtz C., Haldin C.-H.;			
RT	"cDNA cloning and expression of a human platelet-derived growth factor			
RT	(PDGF) receptor specific for B-chain-containing PDGF molecules.;"			
RL	Mol. Cell. Biol. 8:3476-3486(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.243603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Vilaalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schmurch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences.;"			

## ALIGNMENTS

32	1401.5	24.3	960	1	KIT CHICK
33	1401.5	24.3	972	2	Q99562
34	1401.5	24.3	976	1	KIT HUMAN
35	1393.5	24.2	978	2	Q9X593
36	1391.5	24.1	964	2	Q97744
37	1391.5	24.1	975	2	Q7TS86
38	1391	24.1	977	1	KFMS MOUSE
39	1390.5	24.1	964	2	Q9TQ00
40	1390.5	24.1	964	2	Q9TQ01
41	1390.5	24.1	975	2	Q6QJB8
42	1389.5	24.1	976	2	Q6IQ28
43	1389.5	24.1	979	2	Q8CBK9
44	1388.5	24.1	975	2	Q6QJB7
45	1386	24.0	977	2	Q6NXV8

Q08156	gallus gall
Q99662	homo sapien
P10721	homo sapien
Q9x931	canis famil
Q97744	sus scrofa
Q7TS86	mus musculu
P09581	mus musculu
Q9tq00	sus scrofa
Q9tq01	sus scrofa
Q6qjb8	mus musculu
Q6iq28	homo sapien
Q8cbk9	mus musculu
Q6qjb7	mus musculu
Q6nxv8	mus musculu

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP SEQUENCE OF 548-569 FROM N.A.  
 RX MEDLINE=97429921; PubMed=9285559; DOI=10.1038/sj.onc.1201267;  
 RA Chi K.D., McGhee R.A., Wagner A.S., Dietz J.J., Pantazis P.,  
 RA Goustin A.S.;  
 RT "Integration of proviral DNA into the PDGF beta-receptor gene in HTLV-  
 RT I-infected T-cells results in a novel tyrosine kinase product with  
 RT transforming activity";  
 RL Oncogene 15:1051-1057(1997).  
 RN [5]  
 RP SEQUENCE OF 1046-1106 FROM N.A.  
 RX MEDLINE=89028677; PubMed=2846185; DOI=10.1016/0092-8674(88)90224-3;  
 RA Roberts W.M., Look A.T., Roussel M.F., Sherr C.J.;  
 RT "Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor  
 RT genes";  
 RL Cell 55:655-661(1988).  
 RN [6]  
 RP SEQUENCE OF 33-47.  
 RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites";  
 RL Protein Sci. 13:2819-2824(2004).  
 RN [7]  
 RP AUTOPHOSPHORYLATION SITES.  
 RX MEDLINE=89376563; PubMed=2550144; DOI=10.1016/0092-8674(89)90510-2;  
 RA Kazianka A., Cooper J.A.;  
 RT "Autophosphorylation of the PDGF receptor in the kinase insert region  
 RT regulates interactions with cell proteins";  
 RL Cell 58:1121-1133(1989).  
 RN [8]  
 RP INTERACTION WITH APS.  
 RX MEDLINE=99142932; PubMed=9989826; DOI=10.1038/sj.onc.1202326;  
 RA Yokouchi M., Wakioka T., Sakamoto H., Yasukawa H., Ohtsuka S.,  
 RA Sasaki A., Ohtsubo M., Valius M., Inoue A., Komiyama S., Yoshimura A.;  
 RT "APS, an adaptor protein containing PH and SH2 domains, is associated  
 RT with the PDGF receptor and c-Cbl and inhibits PDGF-induced  
 RT mitogenesis";  
 RL Oncogene 18:759-767(1999).  
 RN [9]  
 RP CHROMOSOMAL TRANSLOCATION WITH TRIP11.  
 RX MEDLINE=98043615; PubMed=9373237;  
 RA Abe A., Emi N., Tanimoto M., Terasaki H., Marunouchi T., Saito H.;  
 RT "Fusion of the platelet-derived growth factor receptor beta to a novel  
 RT gene CEV14 in acute myelogenous leukemia after clonal evolution";  
 RL Blood 90:4271-4277(1997).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.79 ANGSTROMS) OF 751-755 IN COMPLEX WITH  
 RP PIK3R1, AND COMPARISON WITH NMR ANALYSIS.  
 RX MEDLINE=21450159; PubMed=11567151; DOI=10.1107/S0907444901012434;  
 RA Paupit R.A., Dennis C.A., Derbyshire D.J., Breeze A.L., Weston S.A.,  
 RA Rowse S., Murshudov G.N.;  
 RT "NMR trial models: experiences with the colicin immunity protein Im7  
 RT and the p85alpha C-terminal SH2-peptide complex";  
 RL Acta Crystallogr. D 57:1397-1404(2001).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1102-1106 IN COMPLEX WITH  
 RP SLCA3R1 AND PDGFRA.  
 RX MEDLINE=22013966; PubMed=11882663; DOI=10.1074/jbc.M201507200;  
 RA Karthikeyan S., Leung T., Ladias J.A.A.;  
 RT "Structural determinants of the Na+/H+ exchanger regulatory factor  
 RT interaction with the beta 2 adrenergic and platelet-derived growth  
 RT factor receptors";  
 RL J. Biol. Chem. 277:18973-18978(2002).  
 CC -1- FUNCTION: Receptor that binds specifically to PDGFR and has a  
 CC tyrosine-protein kinase activity. Phosphorylates Tyr residues at  
 CC the C-terminus of PTEN1 creating a binding site for the SH2  
 CC domain of GRB2.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBUNIT: Homodimer, and heterodimer with PDGFRA. Interacts with  
 CC APS.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- DISEASE: Involved in a form of chronic myelomonocytic leukemia  
 CC (CMML) characterized by abnormal clonal myeloid proliferation and  
 CC by progression to acute myelogenous leukemia (AML) through a  
 CC chromosomal translocation t(5;12)(q33;p13) that involves PDGFRB  
 CC and ETV6/TEL.  
 CC -1- DISEASE: Involved in a acute myelogenous leukemia through a  
 CC chromosomal translocation t(5;14)(q33;q32) that involves PDGFRB  
 CC and TRIP11. The fusion protein may be involved in clonal evolution  
 CC of leukemia and eosinophilia.  
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF  
 CC receptor subfamily.  
 CC -1- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; J03278; AAA60049.1; -;  
 DR EMBL; M21616; AAA36427.1; -;  
 DR EMBL; U33172; AAC51675.1; -;  
 DR EMBL; BC032224; AAH32224.1; -;  
 DR PIR; A28206; PFHUGB  
 DR PDB; 1GQ5; X-ray; A=1102-1106.  
 DR PDB; 1H90; X-ray; B=751-755.  
 DR PDB; 1LWP; Model; A=600-962.  
 DR Genew; HGNC:8804; PDGFRB.  
 DR H-InvDB; HIX0005310; -;  
 DR MIM; 173410; -;  
 DR GO; GO:0004992; F:platelet activating factor receptor activity; TAS.  
 DR GO; GO:0005017; F:platelet-derived growth factor receptor act. .; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001824; RecepttyrkinIII.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR Pfam; PF00047; ig; 2.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR01832; VEGFRECEPTOR. 2.  
 DR ProDom; PD000001; Prot\_kinase; 2.  
 DR SMART; SM00408; IGC2; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS0835; IG LIKE; 2.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
 DR 3D-structure; ATP-binding; Chromosomal translocation;  
 KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;  
 KW Phosphorylation; Proto-oncogene; Receptor; Repeat; Signal;  
 KW Transferrase; Transmembrane; Tyrosine-protein kinase.  
 FT SIGNAL 1 32  
 FT CHAIN 33 1106 Beta platelet-derived growth factor  
 FT receptor.  
 FT Extracellular (Potential).  
 FT Potential.  
 FT Cytoplasmic (Potential).  
 FT Protein kinase.  
 FT Breakpoint for translocation to form  
 FT TRIP11-PDGFRB.  
 FT NP\_BIND 606 614 ATP (By similarity).  
 FT BINDING 634 634 ATP (By similarity).  
 FT ACT\_SITE 826 826 By similarity.  
 FT MOD\_RES 751 751 Phosphotyrosine (by autocatalysis).  
 FT MOD\_RES 857 857 Phosphotyrosine (by autocatalysis).



FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).  
Query Match 99.9%; Score 5762; DB 1; Length 1106;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRLPGAMPALAKGELLALLSLLLELPQISQGLVVTTPPGPELVNVSTFVLTCSGAPV 60  
Db 1 MRLPGAMPALAKGELLALLSLLLELPQISQGLVVTTPPGPELVNVSTFVLTCSGAPV 60  
Qy 61 WERNSEPPQEMAKAQDGTSSVLTNLTLGLDTGEYFCTHNDSRGLETDERKRLIFV 120  
Db 61 WERNSEPPQEMAKAQDGTSSVLTNLTLGLDTGEYFCTHNDSRGLETDERKRLIFV 120  
Qy 121 PDPTVGLPNDARELFIFLFEITITPCRVTDQVLVTLHEKKGDVALPVYDHOGRFS 180  
Db 121 PDPTVGLPNDARELFIFLFEITITPCRVTDQVLVTLHEKKGDVALPVYDHOGRFS 180  
Qy 181 GIFEDRSYICKTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQENITLMCIIGN 240  
Db 181 GIFEDRSYICKTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQENITLMCIIGN 240  
Qy 241 DVNFEWYPRKESGRVPEVPTDPLDMPYHRSILHIPSAELEDSTGTYCNVTESVNDH 300  
Db 241 EVNFEWYPRKESGRVPEVPTDPLDMPYHRSILHIPSAELEDSTGTYCNVTESVNDH 300  
Qy 301 ODEKAINITVSEGYVRLLEGEVGLQFAELHRSSTQVFEAYPPPTVLMFKNRTLGDS 360  
Db 301 ODEKAINITVSEGYVRLLEGEVGLQFAELHRSSTQVFEAYPPPTVLMFKNRTLGDS 360  
Qy 361 SAGEIALSTNVSTRVYSELTVRVKVAAGHYTMRAFEDAEVQLSFQQLINVPVRVL 420  
Db 361 SAGEIALSTNVSTRVYSELTVRVKVAAGHYTMRAFEDAEVQLSFQQLINVPVRVL 420  
Qy 421 ELSSEHPDSGEQVRCRGRMPQBNIIWSACRDLKRCPRELPPTLLGNSSEESQLETVN 480  
Db 421 ELSSEHPDSGEQVRCRGRMPQBNIIWSACRDLKRCPRELPPTLLGNSSEESQLETVN 480  
Qy 481 TYWEEEEFEVSTRLQHVDRPLSVRCLRNAGVQDTQEVIVVPHSLPKVNVISAILA 540  
Db 481 TYWEEEEFEVSTRLQHVDRPLSVRCLRNAGVQDTQEVIVVPHSLPKVNVISAILA 540  
Qy 541 LVLTITLSLILIMLQKPRYERLWKVIESVSDGHEIYVDPMLPYDSTWELPRDQL 600  
Db 541 LVLTITLSLILIMLQKPRYERLWKVIESVSDGHEIYVDPMLPYDSTWELPRDQL 600  
Qy 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVVMLKSTARSSEKQALMSELKIMSHLGP 660  
Db 601 VLGRITLGSAGFGQVVEATAHGLSHSQATMKVAVVMLKSTARSSEKQALMSELKIMSHLGP 660  
Qy 661 HLANVNLGACTGGPIYIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPSPAEVLSNAL 720  
Db 661 HLANVNLGACTGGPIYIITEYCRYGDLVDYLHRNKHTFLOHSDKRRPSPAEVLSNAL 720  
Qy 721 PVGLPLPSHVSLSLTGESDGYMDSKDSVDYVPMMLDMKGDVKVADIENSNMAYPDYNYVP 780  
Db 721 PVGLPLPSHVSLSLTGESDGYMDSKDSVDYVPMMLDMKGDVKVADIENSNMAYPDYNYVP 780  
Qy 781 SAPERTCRATLINESPVLSDYMDLVFGSYQVANGMEFLASKNCVHRDLAARNVLICEKLV 840  
Db 781 SAPERTCRATLINESPVLSDYMDLVFGSYQVANGMEFLASKNCVHRDLAARNVLICEKLV 840  
Qy 841 KICDFGLARDIMRDSNYISKSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900  
Db 841 KICDFGLARDIMRDSNYISKSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG 900  
Qy 901 GTPYPELPMNEQFYNALKRGYRMAQPAHASDEIYIEMQKWEKFEIRPPFSQVLVLLER 960  
Db 901 GTPYPELPMNEQFYNALKRGYRMAQPAHASDEIYIEMQKWEKFEIRPPFSQVLVLLER 960  
Qy 961 LLGEGYKKKYQQVDDEFLRSDHPAILRSQARLPGFHLGRSPDLTSSVLYTAVQNEGDND 1020  
Db 961 LLGEGYKKKYQQVDDEFLRSDHPAILRSQARLPGFHLGRSPDLTSSVLYTAVQNEGDND 1020

Db 961 LLGEGYKKKYQQVDDEFLRSDHPAILRSQARLPGFHLGRSPDLTSSVLYTAVQNEGDND 1020  
Qy 1021 YIIPLPDPKPEVADGEGPLGSPSLASSTLNEVNTSSTISCDSPLEPODEPEPEQLELOV 1080  
Db 1021 YIIPLPDPKPEVADGEGPLGSPSLASSTLNEVNTSSTISCDSPLEPODEPEPEQLELOV 1080  
Qy 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106  
Db 1081 EPEPELEQLPDSGCPAPRAEAEDSFL 1106  
RESULT 2  
Q6QNF3  
ID Q6QNF3 PRELIMINARY; PRT; 1103 AA.  
AC Q6QNF3  
DT 05-JUL-2004 (T-REMBLrel. 27, Created)  
DT 05-JUL-2004 (T-REMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (T-REMBLrel. 27, Last annotation update)  
DE Platelet-derived growth factor receptor beta.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Liao A.T., Chien M.B., London C.A.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-  
CC 1/PDGF receptor subfamily.  
DR HMBP; AY52634; AAS48371.1; -.  
DR HMBP; P11362; IAGW.  
DR GO: 0016021; C: integral to membrane; IEA.  
DR GO: 0005524; F: ATP binding; IEA.  
DR GO: 0004574; F: protein serine/threonine kinase activity; IEA.  
DR GO: 0004872; F: receptor activity; IEA.  
DR GO: 0016740; F: receptor activity; IEA.  
DR GO: 0006458; F: protein amino acid phosphorylation; IEA.  
DR GO: 0007169; P: transmembrane receptor protein tyrosine kin. .; IEA.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003598; IG\_c2.  
DR InterPro: IPR011009; Kinase like.  
DR InterPro: IPR000719; Prot kinase.  
DR InterPro: IPR001824; RecepttyrkinIII.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR InterPro: IPR008266; Tyr\_pkinase\_AS.  
DR InterPro: IPR009134; VEGFR.  
DR Pfam: PF00047; ig; 2.  
DR PRINTS: PR01832; VEGFRECEPTOR.  
DR ProDom: PD000001; Prot\_kinase; 2.  
DR SMART: SM00409; IG; 3.  
DR SMART: SM00408; IGC2; 3.  
DR SMART: SM00220; S\_TKc; 1.  
DR SMART: SM00219; TYR\_Kc; 1.  
DR PROSITE: PS00835; IG-LIKE; 2.  
DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN 1.  
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.  
DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.  
DR PROSITE: PS00240; RECEPTOR TYR\_KIN III; 1.  
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;  
KW Phosphorylation; Receptor; Transferase; Transmembrane.  
SQ SEQUENCE 1103 AA; 123021 MW; A3D66E78A34C5FE0 CRC64;  
Query Match 90.3%; Score 5206.5; DB 2; Length 1103;  
Best Local Similarity 90.1%; Pred. No. 6.7e-305;  
Matches 998; Conservative 43; Mismatches 60; Indels 7; Gaps 3;  
Qy 1 MRLPGAMPALAKGELLALLSLLLELPQISQGLVVTTPPGPELVNVSTFVLTCSGAPV 60  
Db 1 MRLPGAMPALAKGELLALLSLLLELPQISQGLVVTTPPGPELVNVSTFVLTCSGAPV 60

QY 61 VWRMSQEPQEMAKAQDGTFSVLTITLNLGLDTGTYFCTHNDNRGLTDERKRLYIFV 120  
Db 61 VWRMSQEPQEMAKAQDGTFSVLTITLNLGLDTGTYFCTHNDNRGLTDERKRLYIFV 120  
QY 121 PDPTGFLPNDAELFIPLTEITIPCRVTPDQLVLTILHEKKGDVALPVPYDHQGRFS 180  
Db 121 PDPTGFLPNDAELFIPLTEITIPCRVTPDQLVLTILHEKKGDVALPVPYDHQGRFS 180  
QY 181 GTFEDSKYKTTIGREVDSDAYVYRLOVSSINVSNAVQTVRQGENITLMCIIGN 240  
Db 181 GTFEDSKYKTTIGREVDSDAYVYRLOVSSINVSNAVQTVRQGENITLMCIIGN 240  
QY 241 DVNFWFYPRKSGRLVEPVTDPLDMPHRSILHIPSAAELDGGTYTCNVTSVNDH 300  
Db 241 DVNFWFYPRKSGRLVEPVTDPLDMPHRSILHIPSAAELDGGTYTCNVTSVNDH 300  
QY 301 QDEKAINITVSGYVRLLEGEVTLQFAELHRSRTLQVFEAYPPPTVLMFKDNRITLGD 360  
Db 301 QDEKAINITVSGYVRLLEGEVTLQFAELHRSRTLQVFEAYPPPTVLMFKDNRITLGD 360  
QY 361 SAGEIALSTRNVSETRVYSELTLVRUKVABAGHYTMRAFHEDAEVQLSFOLOINVRVL 420  
Db 361 SAGEIALSTRNVSETRVYSELTLVRUKVABAGHYTMRAFHEDAEVQLSFOLOINVRVL 420  
QY 421 ELSESHPDSCQTVRCRGRGMPQPNITWSACRDLKRCPRELPTLLGNSSEESQLETNV 480  
Db 421 ELSESHPDSCQTVRCRGRGMPQPNITWSACRDLKRCPRELPTLLGNSSEESQLETNV 480  
QY 481 TYWEEQEPFVSTLRQLQVDRPLSVRCVTLRNAGVQDTQEVIVVPHSLPKVQVVISAILA 540  
Db 481 TYWEEQEPFVSTLRQLQVDRPLSVRCVTLRNAGVQDTQEVIVVPHSLPKVQVVISAILA 540  
QY 541 LVVLTITISILILMLQKRYEIRWKVIESVSDGHEIYVDPMLQPYDSTWELPRDQL 600  
Db 541 LVVLTITISILILMLQKRYEIRWKVIESVSDGHEIYVDPMLQPYDSTWELPRDQL 600  
QY 601 VLGRITLGSAGFGQVVEATAGLSHQATMKVAVKMLKSTARSEKQALMSKIMSHLGP 660  
Db 601 VLGRITLGSAGFGQVVEATAGLSHQATMKVAVKMLKSTARSEKQALMSKIMSHLGP 660  
QY 661 HLANVNLGACTGGPIYITTECRYGDLVDYLHNRKHTFLQHSKRRPSPSAELYSNAL 720  
Db 661 HLANVNLGACTGGPIYITTECRYGDLVDYLHNRKHTFLQHSKRRPSPSAELYSNAL 720  
QY 721 PVGLPLPSHVSITGESDGYMDKSDSDYVPMKMGKVDYADIESSNYMAPYDNYVP 780  
Db 721 PVGLPLPSHVSITGESDGYMDKSDSDYVPMKMGKVDYADIESSNYMAPYDNYVP 780  
QY 781 SAPERTCRATLINESPVLSDYVANGMEFLASKNCVHRDLAARNVLICGKLV 840  
Db 781 SAPERTCRATLINESPVLSDYVANGMEFLASKNCVHRDLAARNVLICGKLV 840  
QY 841 KICDFGLARDIMRDSNYISKSTFLPLKMWAPESIFNSLYTTLSDVMSFGILLWEITLIG 900  
Db 841 KICDFGLARDIMRDSNYISKSTFLPLKMWAPESIFNSLYTTLSDVMSFGILLWEITLIG 900  
QY 901 GTPYPELPNMEQFNATKRGYMAQPAHASDEIYEIMOKCWEKFEIRPFSQVALLER 960  
Db 901 GTPYPELPNMEQFNATKRGYMAQPAHASDEIYEIMOKCWEKFEIRPFSQVALLER 960  
QY 961 LLGEGYKKYQVDEEFLRSDHAPLRSQARLPFGHLGRSPLDTSSVLYTAVQPNEGDND 1020  
Db 961 LLGEGYKKYQVDEEFLRSDHAPLRSQARLPFGHLGRSPLDTSSVLYTAVQPNEGDND 1020  
QY 1021 YIIPLPDPKPEVADGFLGSPSLASSTLNEVNTSSTISCDSPLEPOD--EPPEPQLEL 1078  
Db 1021 YIIPLPDPKPEVADGFLGSPSLASSTLNEVNTSSTISCDSPLEPOD--EPPEPQLEL 1078  
QY 1079 QVPEPELEQLPDSCGCPAABAEADSFL 1106  
Db 1080 QVPEPELEQLPDSCGCPAABAEADSFL 1106

RESULT 3  
PGDR RAT  
ID PGDR RAT STANDARD; PRT; 1097 AA.  
AC Q05030; Q8R406; Q925F7;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Beta platelet-derived growth factor precursor (EC 2.7.1.112)  
DE (PDGF-R-beta).  
GN Names=PDGfrb;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RA Wang Y., Cult M.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 35-533 FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=93305723; PubMed=8318539; DOI=10.1016/0167-4781(93)90127-Y;  
RA Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;  
RT "Conservation in sequence and affinity of human and rodent PDGF  
ligands and receptors."  
RL Biochim. Biophys. Acta 1173:294-302(1993).  
RN [3]  
RP SEQUENCE OF 528-1090 FROM N.A.  
RC STRAIN=Wistar;  
RX MEDLINE=21359359; PubMed=11346654; DOI=10.1074/jbc.M102995200;  
RA Okuyama H., Shimabara Y., Kawada N., Seki S., Kristensen D.B.,  
RY Yoshizato K., Uyama N., Yamaoka Y.;  
RT "Regulation of cell growth by redox-mediated extracellular proteolysis  
of platelet-derived growth factor receptor beta."  
RL J. Biol. Chem. 276:28274-28280(2001).  
CC -!- FUNCTION: Receptor that binds specifically to PDGFB and has a  
tyrosine-protein kinase activity. Phosphorylates Tyr residues at  
the C-terminus of PTPN11 creating a binding site for the SH2  
domain of GRB2 (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
tyrosine phosphate.  
CC -!- SUBUNIT: Homodimer, and heterodimer with PDGFRA.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF  
receptor subfamily.  
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
EMBL; AV090783; AAM09098.1; -  
EMBL; Z14119; CAA78489.1; -  
EMBL; AF359356; AAK43716.1; -  
PIR; S33766; S33766.  
DR HSSP; P17948; IQSV.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001824; RecepttyrkinIII.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR InterPro; IPR008266; Tyr\_kinase\_AS.  
DR InterPro; IPR009134; VEGFR.  
DR Pfam; PF000047; ig\_3.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR01832; VEGFRECEPTOR.  
DR

DR	ProDom; PD000001; Prot_kinase; 2.	
DR	SMART; SM00408; IGC2; 1.	
DR	SMART; SM00219; TyKc; 1.	
DR	PROSITE; PS00835; IG LIKE; 3.	
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.	
DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.	
DR	PROSITE; PS00109; PROTEIN KINASE TYR; 1.	
DR	PROSITE; PS00240; RECEPTOR TYR_KIN III; 1.	
KW	ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;	
KW	Receptor; Repeat; Signal; Transmembrane;	
KW	Tyrosine-protein kinase.	
FT	SIGNAL	1 31
FT	CHAIN	32 1097
FT	DOMAIN	32 532
FT	TRANSMEM	533 555
FT	DOMAIN	32 119
FT	DOMAIN	128 209
FT	DOMAIN	213 308
FT	DOMAIN	415 523
FT	DOMAIN	599 961
FT	NP BIND	613 613
FT	ACT_SITE	825 825
FT	BINDING	633 633
FT	DISULFID	53 99
FT	DISULFID	148 189
FT	DISULFID	234 290
FT	DISULFID	435 507
FT	MOD_RES	750 750
FT	MOD_RES	856 856
FT	CARBOHYD	44 44
FT	CARBOHYD	88 88
FT	CARBOHYD	102 102
FT	CARBOHYD	214 214
FT	CARBOHYD	291 291
FT	CARBOHYD	306 306
FT	CARBOHYD	353 353
FT	CARBOHYD	370 370
FT	CARBOHYD	444 444
FT	CARBOHYD	467 467
FT	CARBOHYD	478 478
SQ	SEQUENCE	1097 AA; 122827 MW; 56540FA0C5CF22B CRC64;
Query Match		
Best Local Similarity		
Matches 950; Conservative 69; Mismatches 78; Indels 9; Gaps 2;		
QY	1 MRLPGAMPALALGELLLSLLLEPQISQGLVVTTPPGPELVNVSSTFVLTCSSAPV	60
DB	1 MGLPEVMPASVLRGQLLF-VLLLLGQISQGLVITPPGPELVNVSSTFVLTCSSAPV	59
QY	61 VWRMSQEPQEWAKAQDFTSSVLITNTLTGLDTGTFCTHNDNRGLTDERKRLYIFV	120
DB	60 MWEQMSQVPQEAAMNQDFTSSVLITNTVGTGTFYFCVYNNSLGPELSERKRIYIFV	119
QY	121 PDPTVGLPNDABELFLTEITETPCRVTPQVLVTLHEKKGDVALPVVDHQRGFS	180
DB	120 PDPTMGLPMDSEDLFVFDVDTTTPCRVTPQLEVTTLHEKKVDIPLHVPVDHQRGFI	179
QY	181 GIFEDRSYIKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVROGENITLMCIIGN	240
DB	180 GTFEDKTYIKTTIGDREVDSDYVYVSLQVSSINVSNAVQTVVROGESITRIVMGN	239
QY	241 DVNFEWTPRKSGRLVPEVTPFLDMPHYRILHPSAELEDSGTTCNVTVESVNDH	300
DB	240 DVNFWQTPRKSGRLVPEVTPDVLFGVPSRIGSILHIPTAELSDSGTYTCNVSVSNDH	299
QY	301 QDEKATNITVSGYVLLGEVCTLOFAELHRSTLQVFEAYPPPTVLFKQNTLGD	360
DB	300 GDEKAINVTVIENGYVRLLETEDVQIAELHRSTLQVFEAYPTPSVLFKQNTLGD	359

QY	361 SAGEIALSTRNVSETRYVSELTLVRVKVABAGHYTMAAPHEDAEVQLSFQIQINVPVRVL	420
DB	360 SAGELVLSTRNVSETRYVSELTLVRVKVSEAGYYTMAFADQVQLSFQINVPVRVL	419
QY	421 ELSSEHPDSGEOTVRCGRGMPQPNIIWSACRDLKRCRPRELPPTLLGNSSSEESQLETNV	480
DB	420 ELSSEHPANGEQILRCRGRMPQPNVTWTCRDLKRCRKLSPPTPLGNSSKEESQLETNV	479
QY	481 TYWEEEOFEVWSTLRQLQHVDRPLSVRCTLRNAGVQDTQEVIVVPHSLPFKVVVISAILA	540
DB	480 TFWEEDOEYEVWSTLRQLRHVDQPLSVRCMLQNSGRDSQEVTVVPHSLPFKVVVISAILA	539
QY	541 LVVLTIISLIILMLWQKPRYRIRWKVIESVSDSGHEIYVDPMQLPYSTWELPRDQL	600
DB	540 LVVLTVISLIILMLWQKPRYRIRWKVIESVSDSGHEIYVDPVQLPYDSTWELPRDQL	599
QY	601 VLGRITLGSAGFQVVEATAHGLSHSQATMKAVKMLKSTARSEKQALMSELKIMSHLGP	660
DB	600 VLGRITLGSAGFQVVEATAHGLSHSQATMKAVKMLKSTARSEKQALMSELKIMSHLGP	659
QY	661 HLNVMVLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTEFLQHSDDRKRPPSAELYSNAL	720
DB	660 HLNVMVLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTEFLQHSNKHCPSTELYSNAL	719
QY	721 PVGLPLPSHVSLTGESDGYMDMSKDESDYVPMMDMKGVKADIESSNYMAPYDNYVP	780
DB	720 PVGLSLPSHLNLTGESDGYMDMSKDESDYVPMMDMKGHIKYADIESSNYMAPYDNYVP	779
QY	781 SAPERTCRATLINESPVLSDYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	840
DB	780 SAPERTYRATLINDSPVLSYTDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	839
QY	841 KICDFGLARDIMDSNYSIKGSTFPLKWNAPESIFNSLYTTLSDVMSFGILLWEITFLG	900
DB	840 KICDFGLARDIMDSNYSIKGSTFPLKWNAPESIFNSLYTTLSDVMSFGILLWEITFLG	899
QY	901 GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLVLLER	960
DB	900 GTPYPELPMNDQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIRPPFSQVLVLLER	959
QY	961 LLEGYKKYKQVDEEFLRSDHPAILRSQARLPFGHGLRSPDLTSSVLYTAVQNEGDND	1020
DB	960 LLEGYKKYKQVDEEFLRSDHPAILRSQARLPGLSLRSPDLTSSVLYTAVQNETDND	1019
QY	1021 YIIPLPDPKPEVADGEGLESPSLASSTLNEVNTSSTISCDSPLEPODEPEPEQLQV	1080
DB	1020 YIIPLPDPKPEVADGEGLESPSLASSTLNEVNTSSTISCDSPLEQEEP-----QA	1071
QY	1081 EPEPELEQLPDSCCPAPRAEADSFL 1106	
DB	1072 EPEAQLEQPDSCGCPGLAEADSFL 1097	
RESULT 4		
PGDR MOUSE		
ID	PGDR MOUSE	STANDARD; PRT; 1098 AA.
AC	P05622;	
DT	01-NOV-1988 (Rel. 09, Created)	
DT	01-NOV-1988 (Rel. 09, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Beta platelet-derived growth factor receptor precursor (EC 2.7.1.112)	
DE	(PDGF-R-beta).	
GN	Names=PDGfrb; Synonyms=PDGfr;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
RC	TISSUE=Placenta;	
RX	MEDLINE=87014762; PubMed=3020426;	
RA	Yarden Y., Escobedo J.A., Kuang W.-J., Yang-Feng T.L., Daniel T.O.,	
RA	Tremble P.M., Chen E.Y., Ando M.S., Harkins R.N., Francke U.,	











DR	EMBL; BC015186; AAH15186.1; ..	QY	121	PDPVTGFLPNDABELFIFLITEITPCRVTDLPQVLTLEHKKGDVALFVYDHOGRFS	180
DR	PIR; A40162; PFHUGA.	Db	122	PDPAVAFVPLGMDYLVIVDEDDSDALIICRTDPTPTVLHNSG--VVPASVDSRQGFN	179
DR	PDB; 1GQ5; X-ray; ..	QY	181	GIFEDRSYICKTTIGDREVDSDAYVYRLOVSS-INVSNVAVQTVVROQENTLMCIVIG	239
DR	Genew; HGNC:8803; PDGFRA.	Db	180	GTFTVGPYICATVAGKKFQTTIPFNVYALKATSELDLEMEALKTVYKSGETIIVTCAFN	239
DR	MIM; 173490; ..	QY	240	NDVNFEMVYPRKESGR---LVPEVTDFLDDPYHRSITLHIPSARELEDSGYTCNVTS	296
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.	Db	240	NEVVDLQWTPGEVKGKGTMLKEIKVPSIKLVY---TLTVPFATVKGSDGYECAARQA	295
DR	GO; GO:0005018; F:platelet-derived growth factor alpha-recept. . .; TAS.	QY	297	VNDHODEKAINITVWESGVVRLGELGTQFAELHRSRTLQVVFAYPPTVLMFKNRT	356
DR	GO; GO:0002823; P:cell proliferation; TAS	Db	296	TREVKEMKVTISVHEKGIEIKPTFSQLEAVNLHEVHFVVEVRAYPPIRISLKNLT	355
DR	GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.	QY	357	LGDSAGEIALSTRNVSEYVYSELTLRVKVAEAGHYTMRAFHEDAEVQLSFQIQINVP	416
DR	InterPro; IPR007110; Ig-like.	Db	356	LIENTL-EITTDVEKIQEIRYRSKLIIRAKEEDSGHYTIVAQNEADAVKSYTFELLTQVP	414
DR	InterPro; IPR003598; Ig_c2.	QY	417	VRVLELSHSDPS-GEOTVRCGRGMPQNIISACRDLKRCPRELPPTLLGNS-----	469
DR	InterPro; IPR011009; Kinase like.	Db	415	SSILDVDDHGGSTGGTVRCATAGTFELPDIEWMICKDIKKCNNETSWTLANNVNIIT	474
DR	InterPro; IPR000719; Prot_kinase.	QY	470	---SEESOLETNVTVWEEBQEFVNVSTLRLOHVRPLSVRCVTLRNAVGQDTQEVIVPH	526
DR	InterPro; IPR001824; RecepttyrkinIII.	Db	475	EIHSRDRSIVEGRVTF-----AKVETIAVRCLAKNLLGAENRELKLVAP	519
DR	InterPro; IPR001245; Tyr_kinase.	QY	527	SIPFKVVVTSAILALVLTITSLIILIMWQKKPRYIEIRKWKVIESVSSGHEIYVDPNQ	586
DR	InterPro; IPR008266; Tyr_kinase_AS.	Db	520	TLRSELTVAAAVLVLLVIVISLIVLVWIKQPRYIEIRWVIESISPDGHEIYVDPNQ	579
DR	pfam; PF00047; Ig_3.	QY	587	LPVDSFMELPRDLVLRGLSGAGQVVEATAGLSHQAATMKVAVKMLKSTARSEKQ	646
DR	PRINTS; PR01832; VEGFRECEPTOR.	Db	580	LPYDSRWEFPDRGLVLRGLVSGAGVGVGTAGLSRQSPQVWVAVKMLKPTARSEKQ	639
DR	ProDom; PD000001; Prot_kinase; 2.	QY	647	ALMSELKIMSHLGPLHNVNLLGACTKGGPIYIITEYCRYGLVDVLYLHNRKHTFLQHS	706
DR	SMART; SM00408; IGC2; 1.	Db	640	ALMSELKIMTHLGPLHNVNLLGACTKSGPIYIITEYCRYGLVDVLYLHNRKHTFLQHS	699
DR	SMART; SM00219; TyrKc; 1.	QY	707	KRPSPSAEYLYNAL-PVGLPLFVSHVLTGSDGGYMDMSKDSVDYVPMIDMKGVKYAD	765
DR	PROSITE; PS50835; IG LIKE; 2.	Db	700	K---PKELDIIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQVPMLEKEVSKYSD	756
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.	QY	766	IESSNVMAVYDNPVPSAPERTCRATLINE-SPVLSYMDLVGFYSQVANGMEFLASKNCVH	824
DR	PROSITE; PS00101; PROTEIN KINASE_DOM; 1.	Db	757	IQSLYDRPASVYKKSMLDSEVKNLLSDNNSGLTLLDLLSFTYQVARGNEFLASKNCVH	816
DR	PROSITE; PS00109; PROTEIN KINASE_TTR; 1.	QY	825	RLAARNVLLICEGLVKICDFGLARDIMRDSNYISKGSTFLPLKMWAPESIFNSLYTTL	884
DR	PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.	Db	817	ROLAARNVLLAQGKI VKICDFGLARDIMHDSNVYSGSTFLPVKMWAPESIFPNLYTTL	876
KW	3D-structure; Alternative splicing; ATP-binding; Glycoprotein;	QY	885	DVMSFOILLWEITLGGTGYPELPMNEQYNAIKRGYMAQPAHADEIYEIMQKWEK	944
KW	Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;	Db	877	DVMSYGIILLWEIFSLGGTGYPGMMVDSTFYFNKIKSGYRMAKPDHATSEYVEIMVKW	936
KW	Transferrase; Transmembrane; Tyrosine-protein kinase.	QY	945	FEIRPFPSOLVLLERLLGEGYKQYQVDEBEFLRSDHPAILRSQARLPQFHLGRPLDT	1004
FT	SIGNAL 1 23	Db	937	PEKRPFYHLSEIVENLPGQYKSYEKIHLDFLKSDFHFAVAMR-----VDS	984
FT	CHAIN 24 1089	QY	1005	SSVLYTAVQPN-----GDNDYIITPLP--DPKPEVADGPLEGSPSLA	1045
FT	DOMAIN 24 524	Db	985	DNAYIGVTKNEEDKLDKWEGLDEQRLSADSGYIIPDPIDPVPPEEDLKGKRNHSSQT	1044
FT	TRANSMEM 525 549	QY	1046	S---STLNVENTSTISCDSPLEQDEPEPEPELOVEPEPELOLPDSCGCPAPRAEAD	1103
FT	DOMAIN 550 1089	Db	1045	SEESATETGSSSTF-----IKREDE-----TIE---DIDMDDIGIDSSDL-VED	1086
FT	DOMAIN 24 113	QY	1104	SFL 1106	
FT	DOMAIN 202 306	Db	1087	SFL 1089	
FT	DOMAIN 319 410				
FT	DOMAIN 593 954				
FT	DOMAIN 1041 1087				
FT	NP_BIND 599 607				
FT	NP_BIND 627 627				
FT	ACT_SITE 818 818				
FT	MOD_RES 849 849				
FT	CARBOHYD 42 42				
FT	CARBOHYD 76 76				
FT	CARBOHYD 103 103				
FT	CARBOHYD 179 179				
FT	CARBOHYD 353 353				
FT	CARBOHYD 359 359				
FT	CARBOHYD 458 458				
FT	CARBOHYD 468 468				
FT	VARSPLIC 210 218				
FT	VARSPLIC 219 1089				
FT	SEQUENCE 1089 AA; 122669 MW; 5E3FB9940ACD1BE8 CRC64;				

Query Match 40.88; Score 2351.5; DB 1; Length 1089;  
 Best Local Similarity 44.08; Pred. No. 7.8e-133;  
 Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;  
 8 PALAKGELL-LSLLLLEPQISQGLVTPPGPELVNLSVTLTCSGAPVWME-RM 65  
 6 PAFVLGCLLTGLSLILC---QLSLPSIL-PNENEKVQVQLNSFSRLRCFGESEVSWQYPM 61  
 66 SQPPQEM----AKAQDTSSVLTTLNLTGLDTGEYFCHTNDNRGLTDP-ERKRLYIFV 120  
 62 SEESDVEIRNEENNSGLFVLEVSASAAHTGLTYTCYNHTQTBEENLEGRHIYIV 121





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Db 706 DLDIFGLNPADESTRSVYILSPENNGDYMCKQADTMQVYVPMLEKPEKSYSDIQRSLYD 765
QY 773 APVDNVPSAPERTCRATLINES-PVLSYNDLVGFSYQVANGMEFLASKNVCVHRDLAARN 831
Db 766 RPAS--YKKKPLSEVNKILSDDFEGTGLVLDLSTYQVARGMEFLASKNVCVHRDLAARN 823
QY 832 VLICEGKVKICDFGLARDIMRDSNVYKSGSTPLPKWMAPEISPLNSLYTTLSDDVMSFGI 891
Db 824 VLLAHGKVKICDFGLARDIMHDSNVYKSGSTPLPKWMAPEISPLNSLYTTLSDDVMSFGI 883
QY 892 LWEIFTLGGTPTPELPMNEQFYNAIKRGYMAQPAHASDEIYIEMQKWEKEFEIRPPF 951
Db 884 LWEIFSLGGTPTPGMIVDSTFYNKIKSGYMAKPDHATHEVYDINVCKWSEPEKRPSP 943
QY 952 SQVLVLERLLGGYKKYQVDEFLRSDHPAILRSQARLPFGHGLRPLDTSSVLYTA 1011
Db 944 RHLSDIVESLLPMEYKRCYETVHLDFLKSHPAVTR-----MRSDSDNSYIGVTV 993
QY 1012 VQNE-----GNDYIILPLDPKPEVADGEPLEGSPSLASSTLNEVNTSST 1057
Db 994 KNEHKWORESGDFEORLSADSGIILPLDIPVSEDE---SKNRHHSQTSSESIAET 1050
QY 1058 ISCDSPLEQDEPEPQLEQVPEPELEQLPDSCGCPAPRAEADSFL 1106
Db 1051 GSSSFTFKEDD-----ETIEDIMDDIGIDSSDL-VEDSFL 1087

RESULT 9
ID Q7ZY71 PRELIMINARY; PRT; 1087 AA.
AC Q7ZY71;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pgfra-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).

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RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSP-
CC 1/PDGF receptor subfamily.
DR EMBL; BC043948; AAH43948.1; -.
DR HSSP; P36888; IRUB.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; ig; 2.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase
SQ SEQUENCE 1087 AA; 122585 MW; 2C094A5FB7C43566 CRC64;

Query Match 40.2%; Score 2317; DB 2; Length 1087;
Best Local Similarity 44.9%; Pred.No.9.4e-131;
Matches 507; Conservative 183; Mismatches 366; Indels 74; Gaps 23;

QY 7 MPALAKGELLILLLLLEPQ--ISQGLVVT--PGPELVNVSTFVLTCGSGAPVVM 62
Db 2 MPAMRAS---LILGCLLIIGPMAILAENPLTIFPKDELQVLAHSSFTLKCTGESEVSW 58
QY 63 ERMSQPPQOE---MAKAQDGTFFSSVLTLTNLDTGCTGTHNDSRGLETD-ERKRL 116
Db 59 QNPNSNPEKQNVVIRSEENNSGLFVSLVLESDASAFDTGLYCYHNHTQTESEISGTDI 118
QY 117 YIFVPDPTVGFLPNDAEELFIFLTFEITIPCRVTDTPQVLTLLHKKKGDAVLPVYDHQ 176
Db 119 YIVVDPNVFPAPGLFDHIIIVVEDESALVPCRTTDPSEVMKNISSRTVFAFYDSK 178
QY 177 RGFSGIFEDRSYICKTIGDREVDSDAYVYRLQVS-SINSVNVAQTVVROQENITLMC 235
Db 179 QGFAGNFPFGSYICETTSNNKMYQTEPIQLQTKATHNISVENAPEKTFMFRAGETAI DC 238
QY 236 IVTGNDVNVFETWYPRKESGRVPEVPTDFLLDMFY-HIRSIHLIPSAELEDSTYTCNVT 294
Db 239 IVLNEDVLDKWTYPGKQGVGIRNVEE--SKVPYQYLVVYTLTLANATTEDSGEYCAVI 296
QY 295 ESVNDHODEKAINITVVEGYSVLLGEVGTLPQAEHLRSRTLOVFEAPPPTVLPFKDN 354
Db 297 HATLDNRVVKTNITVHEKGFIDLEPMFGSEEPANLHEVKSFTVNLHAYETPGFLFKDN 356
QY 355 RTLGDSSAGEIALSTRNVSEITVLRVVKVAEGHVTMEAFHEDAEVQ-LSFOLQI 413
Db 357 RTLSENLT-EITTSIVTTKETRFQSKULIRAKEEDSGLYTIVA-QNDATKSYSFMLQI 414

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FT	CARBOHYD	467	467	N-linked (GlcNac. . .) (Potential).
FT	CONFLICT	150	150	L -> R (in Ref. 2).
FT	CONFLICT	519	519	S -> T (in Ref. 2).
FT	SEQUENCE	1088	1088	AA; 122641 MW; 590CBB0418801E7 CRC64;
QY	Query Match			40.0%; Score 2304; DB 1; Length 1088;
QY	Best Local Similarity			43.8%; Pred. No. 5.7e-130;
QY	Matches	495;	Conservative	191; Mismatches 355; Indels 88; Gaps 24;
QY	12	LKSELALLSLLLEPQISGLVVTTPGPELVNVSTFVLTCGSAFVWVER-MQOE--	68	
QY	14	LTGSLIVCQLLL--PSI-----LPENENEKIVPLSSFSRLCFGSSEVSWQHPMSEED	65	
QY	69	PPQEMAKAQDGT--FSSVLTLTNLTGLDTCYEYCTHNDSGLETD--ERKELXIFVDPDPTV	125	
QY	66	PNVEIRTEENSSLFVTLEVNASAAHTGYTCYNNHTQTESEIEGRIIYIIVDPDM	125	
QY	126	GLPNDAAELFIETITEITPCRTVDPOLVVTLHEKKGDAVALPVYDHQGFSGIFED	185	
QY	126	AFVPLGWTDSLVIEEDDSAIIECLTDPDTEVTLH--NNGRLVPAVSYSRQGFNGTFSV	183	
QY	186	RSYICKTIGDREVDSDAYVYVQLVSS--INVSNAVQTVVROGENITLMLCIVIGNDVN	244	
QY	184	GPYICATVRGTFKTSFENVYALKATSELNLEMDTRQTVYKAGETIVVTCAVFNNEVD	243	
QY	245	FEWTPY---RKESGRVPEVPTDFLLWPVHIRSILHIPSALAELEDSGTTCNVTESVNDHQ	301	
QY	244	LQWYTGVEVNRKGIIMLEELKPSIKLVY----TLTVPKATVKGSDGYEACAAQAKVEK	239	
QY	302	DEKAINITVVEGYSVRLGVEGTLOFAELHRSRTLQVFEAYPPPTVLMFKNRTLDGSS	361	
QY	300	EMKTVISVHEKGFVQIRPTFGHLETVNLHVQVEFVVEVQAYPTPRISMLKONLTIENL	359	
QY	362	AGEIALSTRNVSETRVSELTUVRKVAEAGHTMTAFHDEAEVQLSFQIQNVPRVLE	421	
QY	360	T-BITTDVQSRQSTRYQSKLKLRAKEEDSGHYTIIVQNDMDKSYTFELSTLVPASILE	418	
QY	422	LSSEHPDS--GEQTVRCGRGMPQNPNIWSACRLKCPRELPTLLGNSSEESQLETVN	480	
QY	419	LVDHGHGSGGQIVRCATGTPLPNIEHMKCKIKCNNDTSWVLA-----SNVSNII	472	
QY	481	TYWEEQEFVSVTLRQLQVDRSLVRLCTLRNVAQDQTEVIVVPHSLPKFVVVISAIA	540	
QY	473	TEFHQRGRSTVEGRVSPAKVEETIAVRCLAKNDLIGNRELKLVAPSLRSELVAVAALV	532	
QY	541	LVLVTISLILILMLQKPRYIRKWRVIESVSDGHEYIYVDPMLPYDSTWELPRDQL	600	
QY	533	LLVIVIVSLVIVLWIKQKPRYIRKWRVIESISPDGHEYIYVDPMLPYDSRWEFPRDGL	592	
QY	601	VLGRTLGSGAFGVWEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGP	660	
QY	593	VLGRILGSGAFGVKVEGTATGLRSQPMKAVKMLKPTARSEKQALMSELKIMTHLGP	652	
QY	661	HLNVNLLGACTGGPIIITTEYCRYGDLVDYLHRNKHTFLQHSKRRPPSAELYSNAL	720	
QY	653	HLNIVNLLGACTSGPIIITTEYCFYGDVLYLHKNRDSPMSRHEK---PKKDLDIFGL	709	
QY	721	PNGLPLPSHVLSTGESDGMKSDKDESVDVYVPMIDMKGVKADYIESSNYMAPYDNYV	779	
QY	710	NPADSTRSVIISFENNGDYVDMKQADTTQYVPMLEKKEVSKYSIDIQRLYDRPASYKK	769	
QY	780	PSAPERTCRATLI--NESPVLSYMDLVGFSYQVANGMEFLASKKNCVHRDLAARNVLI	838	
QY	770	KSMILDSAKNLLSDDDSEGLTLLDLSFTYQVARGMEFLASKKNCVHRDLAARNVLLAQK	829	
QY	839	LVKICDFGLARDIMRDSNYISKSGTFLPLKMAAPESIFNSLYTSLSDVWVSGILLWEIFT	898	
QY	830	IVKICDFGLARDIMHDSNYISKSGTFLPLKMAAPESIFDNLTYTSLSDVWVSGVLLWEIFS	889	
QY	899	LGCTPYPELPMNEOFYNALIKRGYMAQAPAHASDIYEIMOKWEEKIEIPPPSOLVLL	958	
QY	890	LGCTPYPGMMVDSFTFYNKISRGYMAKPDHATSEIVEIMVQCWNSEPEKPSFVHLSEIV	949	
QY	959	ERLLGEGYKKYQVDEEFLRSHDPAILRSQARLPGFHLGRPLDTSSVLYTAVQPN--	1016	
QY	950	ENLLPQYKYSYKHLDFKSDHPAVARMR-----VDSNNAVIGVYKNEED	997	
QY	1017	-----GNDYIIPLP--DPKPEVABEGPLEGSPSLAS--STLNEVNTSST	1057	
QY	998	KLKEWEGGDEQRLGADSGYIIPLDIDVPPEEDLGKRNHSSQTSESAIETGSSST	1057	
QY	1058	ISCDSPLEPQDEPEPPEPQLEQVPEPELEQPDSCCAPRAEAEDSFL	1106	
QY	1058	F-----IKREDE-----TIE-----DIDMDDIGIDSDI-VEDSFL	1088	
QY	Q6E7G6	PRELIMINARY;	PRT;	1079 AA.
QY	Q6E7G6;			
QY	DT	25-OCT-2004 (TREMELrel. 28, Created)		
QY	DT	25-OCT-2004 (TREMELrel. 28, Last sequence update)		
QY	DT	25-OCT-2004 (TREMELrel. 28, Last annotation update)		
QY	DE	Platelet-derived growth factor receptor alpha (Fragment).		
QY	GN	Name=PDGFRA;		
QY	OS	Canis familiaris (Dog).		
QY	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
QY	OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
QY	OX	NCBI_TaxID=9615;		
QY	RN	[1]		
QY	RP	SEQUENCE FROM N.A.		
QY	RA	Dickinson P.J., Roberts B.N., Mallen-StClair J., LeCouteur R.A.;		
QY	RT	Evaluation of Receptor Tyrosine Kinase Expression in Canine Brain		
QY	RT	Tumors.;		
QY	RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.		
QY	RN	[2]		
QY	RP	SEQUENCE FROM N.A.		
QY	RA	Mallen-StClair J., London C.A.;		
QY	RT	"The Role of PDGFRA in Canine Cancer.;"		
QY	RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.		
QY	CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).		
QY	CC	-I- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-		
QY	CC	1/PDGF receptor subfamily.		
QY	DR	EMBL; AY525124; AAS91495.2;		
QY	DR	GO; GO:0016020; C:membrane; IEA.		
QY	DR	GO; GO:0005524; F:ATP binding; IEA.		
QY	DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.		
QY	DR	GO; GO:0004872; F:receptor activity; IEA.		
QY	DR	GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . ; IEA.		
QY	DR	GO; GO:0004668; P:protein amino acid phosphorylation; IEA.		
QY	DR	GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA.		
QY	DR	InterPro; IPR003599; Ig.		
QY	DR	InterPro; IPR007110; Ig-like.		
QY	DR	InterPro; IPR003598; Ig_c2.		
QY	DR	InterPro; IPR011009; Kinase like.		
QY	DR	InterPro; IPR007119; Prot kinase.		
QY	DR	InterPro; IPR001824; RecepttyrkinIII.		
QY	DR	InterPro; IPR002290; Ser_thr_kinase.		
QY	DR	InterPro; IPR001245; Tyr_kinase.		
QY	DR	InterPro; IPR008266; Tyr_kinase_AS.		
QY	DR	InterPro; IPR009134; VEGFR.		
QY	DR	Pfam; PF00047; ig; 2.		
QY	DR	Pfam; PF00069; Pkinase; 1.		
QY	DR	PRINTS; PR01832; VEGPRECEPTOR.		
QY	DR	ProDom; PD000001; Prot kinase; 2.		
QY	DR	SMART; SM00409; IG; 4.		
QY	DR	SMART; SM00408; IGC2; 3.		
QY	DR	SMART; SM00220; S_TKc; 1.		
QY	DR	SMART; SM00219; TyKc; 1.		
QY	DR	PROSITE; PS00835; IG_Like; 2.		
QY	DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.		
QY	DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.		
QY	DR	PROSITE; PS00109; PROTEIN KINASE_TVR; 1.		
QY	DR	PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.		
QY	QW	ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;		
QY	QW	Phosphorylation; Receptor; Transferrase; Transmembrane.		









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DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Platelet-derived growth factor receptor alpha.
GN Name=PDGFR- $\alpha$ ;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20302546; PubMed=10842055; DOI=10.1016/S0925-4773(00)00321-X;
RA Atrialotis P.;
RT in vivo and in vitro.;
RL Mech. Dev. 94:13-24(2000).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to the Tyr family of protein kinases. CSP-
CC 1/PDGFR receptor subfamily.
DR EMBL; AF188842; AAF01460.1; -.
DR HSP; P36888; INJB.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005524; F: ATP binding; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0016740; F: transferase activity; IEA.
DR GO; GO:0005021; F: vascular endothelial growth factor receptor.; IEA.
DR GO; GO:000468; P: protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrknsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferrase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 1087 AA; 122939 MW; F3306BDD3D983E31 CRC64;

Query Match 39.4%; Score 2270; DB 2; Length 1087;
Best Local Similarity 44.1%; Pred. No. 6.4e-128;
Matches 499; Conservative 176; Mismatches 361; Indels 96; Gaps 21;

QY 12 LKGGLLLSLLLEPQISQGLVTPPGPELVNVSSTFVLTCGSGAPVYVWRMSQEPQ 71
DB 15 LTGELLTLCQLP-----PTVPNENNVQVNSNFTLKSGDSEVSN-----QYPT 62

QY 72 EMKAQD-----GTFSSVLTNTLTGLDTGYFCTHNSDRGLETD-ERKRLYIFV 122
DB 63 EGSIRIDIRHEENNSGLFVTLEVGNASAAHTGMVGVYVNHQTQVEDGEVEGKDIYI 122

QY 123 PTVGFLPNDAAELFTITEITETPCRVTPDQLVTLHEKKGVALPVVDHQRFGSI 182
DB 123 PDMPFVPSLPDQFILVEEGDPTIPCKTSDPSAEVTLVNSL-DKPYAFVDSKQGVGN 181

QY 183 FEDRSYICKTIGREVDSDAYYVRLQVSS-INVSNAVQTVVRQGENITLMCIVICND 241
DB 182 FLAGPYCTKVMVGVEFSDEFLYLRLATSQLPVEIEALKTVYKGTETIVTVCVFDNE 241
QY 242 VVNFETVPRKESGRLEVPVTDLLDMP-YHRSILHIPSABLEDSGTTCNVTVESVNDH 300
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242 VVNLQWNPYGVKKEGLIKLDD--IKVPSQKLVVMLTIPDLVVKDTGDECTARHATKEV 299
QY 301 QDEKAINITVVEGTVRLLGEVGTIQPAELHRSRTLQVFEAYPPTVLFKDNKTLGDS 360
DB 300 KENKQWITVHDKGFIHLEPQSPLEAVNLHVKNFVVDVQAYPAKMWLKNVTLLN 359
QY 361 SAGEIATSRNVSETRYVSELTIVRVKVAEAGHYTMRAFHDAEVQSLFQIQINPVRL 420
DB 360 LT-EIVTSNRVQETRFQSVLKLIRAKEDSTILMLLKNEDEIKRYTFSLLIQPALIL 418
QY 421 ELSSEHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS-----S 470
DB 419 DLMDHDSAGSAGTQVRCCLAEGTLPDVEWLKCKIKCSNDTSWTLTNNISDIHMEHL 478
QY 471 EESQLENTVTVWEEQEFVSTLRQLQHVDRPLSVCTLRNAVGDQDTEVIVPHSLPF 530
DB 479 DERNVESQVTF-----QKVEETLAVRCVARNDLGAVTRELKLVAPTILRS 523
QY 531 KVVVISAILALVVLTIISLIILMLWQKPKRYEIRKWKVIESVSSDGEHYIYVDPMLQPYD 590
DB 524 ELTVAAAVLVLVIVISLIVLVIWKQPKRYEIRWVIESIPDGEHYIYVDPMLQPYD 583
QY 591 STWELPRDOLVGLRTLGSGAFQGVVEATAHGUSHQATKVAVKMLKSTARSEKQALMS 650
DB 584 SRWEPDRDLVGLRILGSGAFGVVEGTAYGLSRSPVMKVAVKMLKPTARSEKQALMS 643
QY 651 ELKIMSHLPHLVNVLGACTKGGPIYIITVRYGDLVDYLRNKHFTLQHSDKRRP 710
DB 644 ELKIMTHLPHLVNVLGACTKSGPIYIITVRYGDLVNLHKNRDNFLSRHEK---700
QY 711 PSAELYSNAL-PVGLPLPSHVSILTGESDGGYMDMSKDESVDYVPMIDMKGVKADIESS 769
DB 701 PKKOLDIFGMNPADESTSYVILSPENTGEYMDKQADTTQVPMLEKESKYSIQRS 760
QY 770 NTMAPYDNTVPSAPERTCRATLINE-SPVLVMDLVGFSYOVANGMEFLASKNCVHRDLA 828
DB 761 VYDRPASYYKKSLSESEVKNLLSDGSEGLDLDLSFTYQVARGMEFLASKNCVHRDLA 820
QY 829 ARNVLICEGLVKIKCDFGLARDIMRDSNYISKGSFTPLKMWAPESIFNSLYTTLSDVMS 888
DB 821 ARNVLAQKIKVKICDFGLARDIMHDSNVYSGSFTPLVKKWAPESIFDNLYTTLSDVMS 880
QY 889 FGILLWEITLGTTPPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKWEKFEIR 948
DB 881 YGILLWEIFEISGLIYPCGMVDSFTYFKIKSGYRMAKPDHATNEVYVEIMVKWNEPEKR 940
QY 949 PPSQLVALLERLLGEGYKKYQVDEEFLRSDHPAILRSQARLPGFHGLRSPDTSVVL 1008
DB 941 PSFYHLSEIVESLLPGEYKKYKIEKHLDFKSDHPAVTR-----MRGCDNAYIG 990
QY 1009 YT-----AVQPNB-----GDNDYIIPDPKPEVADEGPLEGSPSLAGSTLNEVNT 1054
DB 991 VTYKEDKIKDRESGFDEQRLSADSGYITPLPDIDPVSEDE---LCKNRHSSQTSSEA 1047
QY 1055 SSTISCDSPLEODEPEPEPQELQVEPEPELQLPDSCGCPAPRAEASFL 1106
DB 1048 IETGSSSTFIKED-----ETIEDIDMDDDIGIDSDL-VEDSFL 1087

RESULT 15
QY Q9DE49 PRELIMINARY; PRT; 1059 AA.
ID Q9DE49
AC Q9DE49;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Platelet-derived growth factor receptor alpha.
GN Name=pdgfra;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
```



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OX NCBI_TaxID=7955;
RN [1]
RP Liu L., Balasubramanian N.V., Ge R.;
RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-
CC 1/PDGF receptor subfamily.
DR EMBL: AF200951.1; AAG43479.1; -.
DR HSP; P36888; IRJB.
DR ZFIN: ZDB-GENE-990415-208; pdgfra.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005524; F: ATP binding; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0016740; F: transferase activity; IEA.
DR GO: GO:0005021; F: vascular endothelial growth factor receptor. . ; IEA.
DR GO: GO:000468; P: protein amino acid phosphorylation; IEA.
DR GO: GO:0007169; P: transmembrane receptor protein tyrosine kin. . ; IEA.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig C2.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000719; Prot.kinase.
DR InterPro: IPR001824; RecepttyrknsIII.
DR InterPro: IPR001245; Tyr.pkinase.
DR InterPro: IPR008266; Tyr.pkinase_AS.
DR InterPro: IPR009134; VEGFR.
DR Pfam: PF00047; Ig. 1.
DR PRINTS: PR01832; VEGFRECEPTOR.
DR ProDom: PD000001; Prot.kinase; 2.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS50835; IG LIKE; 2.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 1059 AA; 118210 MW; 0AE93E2ABD9A72F3 CRC64;

Query Match 38.3%; Score 2210; DB 2; Length 1059;
Best Local Similarity 44.1%; Pred. No. 2.5e-124;
Matches 469; Conservative 179; Mismatches 344; Indels 72; Gaps 18;

QY 27 PQISQGLVTPPGPELVNVSSTFVLTCSSAPVWERMSEQP---PQEMAKQDGTFS 83
DB 6 PQSVQAPLIWPQRESMEVSLHSTRLCRGQTLSW-----NGPVFDDQTNVKKGLFIS 61

QY 84 VLTLTNLTGLDTGEYFCTHNDNRGLTDERKRLYIFVPDPTVGFLPNDABELFIFLFEIT 143
DB 62 TVTISNATAVHTGEVYVCSSEPFNSTES---TIYIVYDPDPTFPVPSMTFENHVLTSYD 117

QY 144 EITIPCRVTDPLVTLHEKKGDVALPVVDHQRGSGIFEDRSYICKTKTIGREVDSDA 203
DB 118 EMEIPCRVTDPSASVSLIHMTDQVMSAYDSKRGFTGLFGAGTYVCRALIHQNHSIE 177

QY 204 YVYVR-LQVSSINVSNAVQTVVRQENITLMCTIVGNDVVNFETWYPRKESGRVPEVT 262
DB 178 YIVHGWGGDLRVLRAVRKRTLLVGVTITVDCVAKGSEVLEDHWKYPGKLANRGPKTVK 237

QY 263 DFLDMPYHIRSLIHPSABLESGTYTCNVVTSVNDHDEKAINITVBSGVYRVLIGE 322
DB 238 ENKLNL--EITYTLTVTNASPKDSGIYACISITDIMSNESQTKELTITVYDHEFVHINPLI 295

QY 323 GTIQFELHRSRTLQVVFAYPPPTVLWFKDNKRTGLDSSAGEIALSTRNVSETRYVSELT 382
DB 296 GPVETARLDEVPBFKVDIESFPAPKVTWLTWSSVLGDDTA-EISTILLIKIGETSYQGVLN 354

QY 383 LVKVKVAEAGHYTMRAFHEDAEVQLSPQLQINPVVRVLELSESHPDGGE-QTVRCRGRGM 441
DB 355 LIRAKAEDSGNVTVAKEIGSISTSYFYLQVQKVPFPIVDLIDVHHGSAAGQEVVCTAGGS 414

442 PPNIIWSACRDLKRCPRE----LPPTLLGNSSEESQLETNVTYTWBEEQFEFVYSTRL 497
415 PFEVDWDICKNLKHCANDSSQWMLPI--NSTDITVELQWNV-----DNHIESHIP 465
498 QHVDRLSVRCTLNAGVQDTQEVIVV---PHSLPFKVVISAILALVLTIIISLIILIM 554
466 HHLEGTVAVRCLARNDMGVSVREVKLMSSGPHS---ELTVAAAVLVLLVILVILVLI 522
555 LWOKPRYEIRWKVIESVSDGHEIYVDPQMLPYDSTWELPRDOLVGLRTGLSGGATGOV 614
523 IWQKPRYEIRWRVIESVSPDGEIYVDPQMLPYDSRWEFFRDGLVGLRVLSGATGKV 582
615 VEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGPLHNVNLLGACTKG 674
583 VEGTAGLSRSQPMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNVNLLGACTKS 642
675 GPIYIITEYCRYGDLVDYLRNKHFTLOHSDKRRPPSAELYSNALPVGLPLPSHVSITG 734
643 GPIYIITEYCFYGLVNYLHKNRDGFLSRHTEKGGKDLDFGIN--PADESSRSYVILSL 700
735 ESDGGYMDMSKDSVDYVPMKMGDKVYADIESNTMAPYDNYVPSAPERTCRA-TLIN 793
701 EKGDTMDMKQADTMQYVPMLEWNEASKYSPIQRSYDHP-----PSHRQFNDEABSLLS 755
794 ESPV--LSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLVKICDFGLARDI 851
756 DDSAEGLTMTDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLSQGKIVKICDFGLARDI 815
852 MRDSNVISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLGGTTPPELPMNE 911
816 MHDNNTVYSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGILLWEIIFSLGGTTPPGMVVDS 875
912 QFYNAIKRGYRMAQPAHASDEIYEIMOKCWEKFEIRPPFSQVLVLLERLLGEGYKKYQ 971
876 SFTNKLKSGYRMTKPEHASDVTYELMMKWNSEPEKRPSPHSLSDTVASLLPSGFKRCYE 935
972 QVDEEFLRSDHPAILRSQARLPGFHLRSLPDTSSVLYTAVQPNEG----- 1017
936 RVNHDFLKSHPAVTRVQC-----IDNDAYVMGVLYKNQGMKTKRESGDFDQRL 984
1018 --DNDYIILPLDPKPEVADEGPLEGSPSLASSTILNEVNTSSTIS 1059
985 SSDSGYIILPLDPLSDNEDYSKRNHRHSQTSSESAIDTGSSES 1028

Search completed: March 11, 2005, 07:17:22
Job time : 150.611 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2005, 05:13:43 ; Search time 142.389 Seconds  
(without alignments)  
3916.424 Million cell updates/sec

Title: US-10-027-400-2

Perfect score: 5652

Sequence: 1 MGTSHPAFLVGLLGLSL.....IDMDDIGIDSSDLVEDSFL 1089

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5652	100.0	1089	1 PGDS HUMAN	P16234 homo sapien
2	5400	95.5	1079	2 Q6E7G6	Q6E7G6 canis famil
3	5232	92.6	1089	2 Q7TSJ3	Q7TSJ3 mus musculu
4	5229	92.5	1089	1 PGDS MOUSE	P26518 mus musculu
5	5190.5	91.8	1088	1 PGDS RAT	P20786 rattus norv
6	4577	81.0	1087	2 Q9PUF6	Q9PUF6 gallus gall
7	4246	75.1	1087	1 PGDS XENLA	P26619 xenopus lae
8	4228	74.8	1087	2 Q7ZY71	Q7ZY71 xenopus lae
9	3715	65.7	743	2 Q6P4H5	Q6P4H5 homo sapien
10	3592	63.6	790	2 Q8C4N3	Q8C4N3 mus musculu
11	3419.5	60.5	1062	2 Q8AXC7	Q8AXC7 fugu rubrip
12	3363	59.5	1059	2 Q9DB49	Q9DB49 brachydanio
13	3296	58.3	1078	2 Q8AXC8	Q8AXC8 fugu rubrip
14	2692	47.6	849	2 Q7Z608	Q7Z608 homo sapien
15	2354.5	41.7	1106	1 PGDR HUMAN	P09619 homo sapien
16	2316.5	41.3	1098	1 PGDR_MOUSE	P05822 mus musculu
17	2327	41.2	1099	2 Q7TMR8	Q7TMR8 mus musculu
18	2326	41.2	1097	1 PGDR RAT	Q05030 rattus norv
19	2285.5	40.4	1103	2 Q6QNF3	Q6QNF3 canis famil
20	2182.5	38.6	1048	2 P79749	P79749 fugu rubrip
21	2132.5	37.7	686	2 Q75WK5	Q75WK5 oryza lat
22	2043	36.1	486	2 Q8CGH8	Q8CGH8 mus musculu
23	1914.5	33.9	457	2 Q90269	Q90269 brachydanio
24	1835.5	32.5	986	2 Q8UVR9	Q8UVR9 fugu rubrip
25	1554.5	27.5	976	2 Q9W755	Q9W755 brachydanio
26	1553.5	27.5	976	2 Q8JPR5	Q8JPR5 brachydanio
27	1527	27.0	984	2 Q8AXC6	Q8AXC6 fugu rubrip
28	1489	26.3	978	1 KIT_CAPIH	P28317 capra hircu
29	1481.5	26.2	977	1 KIT_BOVIN	P43481 bos taurus
30	1472	26.0	964	2 Q97744	Q97744 sus scrofa
31	1472	26.0	964	2 Q9TQO0	Q9TQO0 sus scrofa

32	1470.5	26.0	975	2 Q7YRV7	Q7YRV7 canis famil
33	1469.5	26.0	979	2 Q8WN23	Q8WN23 canis famil
34	1469	26.0	964	2 Q9TQO1	Q9TQO1 sus scrofa
35	1469	26.0	978	2 Q9XS93	Q9XS93 canis famil
36	1463.5	25.9	975	1 KIT_CANFA	Q97999 canis famil
37	1461.5	25.9	960	1 KIT_CHICK	Q08156 gallus gall
38	1460	25.8	974	2 Q63702	Q63702 rattus ratt
39	1458	25.8	978	2 Q63116	Q63116 rattus norv
40	1457.5	25.8	972	2 Q99662	Q99662 homo sapien
41	1454.5	25.7	976	1 KIT_HUMAN	P10721 homo sapien
42	1453.5	25.7	979	2 Q8C8K9	Q8C8K9 mus musculu
43	1452	25.7	972	2 Q761I0	Q761I0 callithrix
44	1450.5	25.7	975	2 Q6QJB8	Q6QJB8 mus musculu
45	1450.5	25.7	975	2 Q7TS86	Q7TS86 mus musculu

## ALIGNMENTS

RESULT 1

ID	PGDS_HUMAN	STANDARD;	PRT;	1089 AA.
AC	P16234; Q96KZ7;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112)			
DE	(PDGF-R-alpha) (CD140a antigen).			
GN	Name=PDGFRA;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=89130149; PubMed=2536956;			
RA	Matsui T., Heidaran M., Miki T., Popescu N., la Rochelle W., Kraus M.,			
RA	Pierce J., Aaronson S.;			
RT	"Isolation of a novel receptor cDNA establishes the existence of two			
RT	PDGF receptor genes.";			
RL	Science 243:800-804(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=89296915; PubMed=2544881;			
RA	Classon-Walsh L., Eriksson A., Westermarck B., Heldin C.H.;			
RT	"CDNA cloning and expression of the human A-type platelet-derived			
RT	growth factor (PDGF) receptor establishes structural similarity to the			
RT	B-type PDGF receptor.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:4917-4921(1989).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Blood;			
RX	MEDLINE=96163874; PubMed=8596421;			
RA	Kawagishi J., Ku T.;			
RT	"Structure, organization, and transcription units of the human alpha-			
RT	platelet-derived growth factor receptor gene, PDGFRA.";			
RL	Genomics 30:224-232(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Placenta;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP DISEASE.  
RX MEDLINE=22547205; PubMed=12660384; DOI=10.1056/NEJMoa025217;  
RA Coors J., DeAngelo D.J., Gotlib J., Stover E.H., Legare R.D.,  
RA Cortes J., Kutok J., Clark J., Galinsky I., Griffin J.D., Cross N.C.,  
RA Tefferi A., Malone J., Alam R., Schrier S.L., Schmid J., Rose M.,  
RA Vandenberghe P., Verhoef G., Boogaerts M., Wlodarska I.,  
RA Kantarjian H., Marynen P., Coutre S.E., Stone R., Gilliland D.G.;  
RT "A tyrosine kinase created by fusion of the PDGFR and FIP1L1 genes as  
RT a therapeutic target of imatinib in idiopathic hypereosinophilic  
RL syndrome.";  
RL N. Engl. J. Med. 348:1201-1214(2003).  
RN [6]  
RX RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1185-1189 IN COMPLEX WITH  
RP SLC9A3R1 AND PDGFRB.  
RA MEDLINE=22013966; PubMed=11882663; DOI=10.1074/jbc.M201507200;  
RX Karthikeyan S., Leung T., Ladias J.A.A.;  
RT "Structural determinants of the Na+/H+ exchanger regulatory factor  
RT interaction with the beta 2 adrenergic and platelet-derived growth  
RT factor receptors.";  
RL J. Biol. Chem. 277:18973-18978(2002).  
CC -1- FUNCTION: Receptor that binds both PDGFA and PDGFB and has a  
CC tyrosine-protein kinase activity.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- SUBUNIT: Homodimer, and heterodimer with PDGFRB.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=P16234-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=P16234-2; Sequence=VSP\_007833, VSP\_007834;  
CC Note=No experimental confirmation available;  
CC -1- DISEASE: A fusion of PDGFR and FIP1L1 (FIP1L1-PDGFR), due to an  
CC interstitial chromosomal deletion, is the cause of some cases of  
CC hypereosinophilic syndrome (HES) [MIM:607685], a rare hematologic  
CC disorder characterized by sustained overproduction of eosinophils  
CC in the bone marrow, eosinophilia, tissue infiltration and organ  
CC damage.  
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF  
CC receptor subfamily.  
CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.  
CC -----  
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CC -----  
CC EMBL; M21574; AAA96715.1; -  
CC EMBL; M22734; AAA60048.1; -  
CC EMBL; D50017; BAA08742.1; -  
CC EMBL; D50002; BAA08742.1; JOINED.  
CC EMBL; D50003; BAA08742.1; JOINED.  
CC EMBL; D50004; BAA08742.1; JOINED.  
CC EMBL; D50005; BAA08742.1; JOINED.  
CC EMBL; D50006; BAA08742.1; JOINED.  
CC EMBL; D50007; BAA08742.1; JOINED.  
CC EMBL; D50008; BAA08742.1; JOINED.  
CC EMBL; D50009; BAA08742.1; JOINED.  
CC EMBL; D50010; BAA08742.1; JOINED.  
CC EMBL; D50011; BAA08742.1; JOINED.

DR EMBL; D50012; BAA08742.1; JOINED.  
DR EMBL; D50013; BAA08742.1; JOINED.  
DR EMBL; D50014; BAA08742.1; JOINED.  
DR EMBL; D50015; BAA08742.1; JOINED.  
DR EMBL; D50016; BAA08742.1; JOINED.  
DR EMBL; BCO15186; AAH15186.1; -  
DR PIR; A40162; PFHUGA.  
DR PDB; 1GQ5; X-ray; -  
DR Genew; HGNC:8803; PDGFRA.  
DR MIM; 173490; -  
DR MIM; 607685; -  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0005018; F:platelet-derived growth factor alpha-recept. .; TAS.  
DR GO; GO:0008283; P:cell proliferation; TAS.  
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_C2.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001824; Recepttyr\_kinIII.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR InterPro; IPR008366; Tyr\_kinase\_AS.  
DR InterPro; IPR009134; VEGFR.  
DR Pfam; PF00047; Ig; 3.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PRO1832; VEGPRECEPTOR.  
DR ProDom; PD000001; Prot\_kinase; 2.  
DR SMART; SM00408; IGC2; 1.  
DR SMART; SM00219; TyrcK; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
DR 3D-structure; Alternative splicing; ATP-binding; Glycoprotein;  
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;  
KW Transferase; Transmembrane; Tyrosine-protein kinase.  
FT SIGNAL 1 23 Alpha platelet-derived growth factor  
FT CHAIN 24 1089 receptor.  
FT DOMAIN 24 524 Extracellular (Potential).  
FT TRANSMEM 525 549 Potential.  
FT DOMAIN 550 1089 Cytoplasmic (Potential).  
FT DOMAIN 24 113 Ig-like C2-type 1.  
FT DOMAIN 202 306 Ig-like C2-type 3.  
FT DOMAIN 319 410 Ig-like C2-type 4.  
FT DOMAIN 593 954 Protein kinase.  
FT DOMAIN 1041 1087 Ser-rich.  
FT NP\_BIND 599 607 ATP (by similarity).  
FT BINDING 627 627 ATP (by similarity).  
FT ACT\_SITE 818 818 By similarity.  
FT MOD\_RES 849 849 Phosphotyrosine (by autocatalysis) (By  
FT similarity).  
FT CARBOHYD 42 42 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 76 76 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 103 103 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 179 179 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 353 353 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 359 359 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 458 458 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 468 468 N-linked (GlcNAc... ) (Potential).  
FT VARSPPLIC 210 218 ATSELDLEM -> GTCTISFLL (in isoform 2).  
FT /FTID=VSP\_007833.  
FT /FTID=VSP\_007834.  
FT VARSPPLIC 219 1089 Missing (in isoform 2).  
FT SEQUENCE 1089 AA; 122669 MW; 5E3FE9940ACD1BE8 CRC64;  
SQ  
Query Match 100.0%; Score 5652; DB 1; Length 1089;  
Best Local Similarity 100.0%; Pred. No. 5.3e-297;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MCTSHPAFLVIGCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQYP 60  
|||||

Db 1 MGTSHPAFLVGLCLTGLSLILCOLSLPSILPNEKVKVQLNSSFSRLCRGSESEVSNQYP 60  
QY 61 MSEEESDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTETEENLEGRHIYY 120  
Db 61 MSEEESDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNHTQTETEENLEGRHIYY 120  
QY 121 VPDPAVAPLGMATDYLIVVEDDSALIPCRITDTPETPTLHNSGVVPASYSRQGFNG 180  
Db 121 VPDPAVAPLGMATDYLIVVEDDSALIPCRITDTPETPTLHNSGVVPASYSRQGFNG 180  
QY 181 TPTVGPVICBATVKGKFFQIPNVVALKATSELDLEMEALKTIVYKSGETIVVTCVFN 240  
Db 181 TPTVGPVICBATVKGKFFQIPNVVALKATSELDLEMEALKTIVYKSGETIVVTCVFN 240  
QY 241 EVDLQWTPGVEKGGITMLEIKVPSIKLVVTLVPEATVXDSGDYECARQATREVK 300  
Db 241 EVDLQWTPGVEKGGITMLEIKVPSIKLVVTLVPEATVXDSGDYECARQATREVK 300  
QY 301 EMKVTISVHEKGFIEIKPTFSQLEAVNLHVKHFVVEVRAYPPIRISMLKNNLTLENL 360  
Db 301 EMKVTISVHEKGFIEIKPTFSQLEAVNLHVKHFVVEVRAYPPIRISMLKNNLTLENL 360  
QY 361 TEITTOVEKIQEIRYRSKULIRAKEDSGHYTIVAQNEADAVKSYTFELLTQVPSILDL 420  
Db 361 TEITTOVEKIQEIRYRSKULIRAKEDSGHYTIVAQNEADAVKSYTFELLTQVPSILDL 420  
QY 421 VDDHSGTGGQVRCVTAEGTLPDIEWMICKOIKKCNNETSWITLANNVSNITIEHSRD 480  
Db 421 VDDHSGTGGQVRCVTAEGTLPDIEWMICKOIKKCNNETSWITLANNVSNITIEHSRD 480  
QY 481 RSTVEGRVTFKVEETIAVCLAKNLLGAENRELKLVAPTRSELVAAVLLVIVII 540  
Db 481 RSTVEGRVTFKVEETIAVCLAKNLLGAENRELKLVAPTRSELVAAVLLVIVII 540  
QY 541 SLIVLVVWKPRIYIRVRVIESIPDGHYIYVDPMLPYDSRNEFRDGLVLRVLG 600  
Db 541 SLIVLVVWKPRIYIRVRVIESIPDGHYIYVDPMLPYDSRNEFRDGLVLRVLG 600  
QY 601 SGAFKVVVGTAYGLSRSPVMKVAVKMLKPTARSSEKQALMSKIMTHLGPLHNVNL 660  
Db 601 SGAFKVVVGTAYGLSRSPVMKVAVKMLKPTARSSEKQALMSKIMTHLGPLHNVNL 660  
QY 661 LGACTKSGPIYIITEYCFYGDLYNHLKNDSPFLSHPEKPKKELDIFGLNPADESTRY 720  
Db 661 LGACTKSGPIYIITEYCFYGDLYNHLKNDSPFLSHPEKPKKELDIFGLNPADESTRY 720  
QY 721 VILSPENNGDYMDKQADTQVYVPMLEKVEKSYDIQSLYDRPASYKKKMLDSEVK 780  
Db 721 VILSPENNGDYMDKQADTQVYVPMLEKVEKSYDIQSLYDRPASYKKKMLDSEVK 780  
QY 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKI VKICDFGLA 840  
Db 781 LLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOGKI VKICDFGLA 840  
QY 841 RIMHDSNVKSGSTFLPKVWMAPEIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGWM 900  
Db 841 RIMHDSNVKSGSTFLPKVWMAPEIFDNLYTTLSDVMSYGILLWEIFSLGCTPYPGWM 900  
QY 901 VDSFTFNKIKSGYMAKPDHATSEVYEMVKWNSPEKRPSPYHLSEIVENLLPQYKK 960  
Db 901 VDSFTFNKIKSGYMAKPDHATSEVYEMVKWNSPEKRPSPYHLSEIVENLLPQYKK 960  
QY 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNEEDKLDKDWEGGLDEQRLSADSGYII 1020  
Db 961 SYEKIHLDFLKSHPAVARMVDSNAYIGVTYKNEEDKLDKDWEGGLDEQRLSADSGYII 1020  
QY 1021 PLPDPIDPVEEDLGRNRRHSQTSSESAIETGSSSSTFIKREDETIEDIMWDDIGIDS 1080  
Db 1021 PLPDPIDPVEEDLGRNRRHSQTSSESAIETGSSSSTFIKREDETIEDIMWDDIGIDS 1080  
QY 1081 SLDVEDSFL 1089  
Db 1081 SLDVEDSFL 1089

## RESULT 2

Q6E7G6 PRELIMINARY; PRT; 1079 AA.  
ID Q6E7G6  
AC Q6E7G6  
DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
DE Platelet-derived growth factor receptor alpha (fragment).  
GN Name-PDGFR;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Dickinson P.J., Roberts B.N., Mallen-StClair J., LeCouteur R.A.;  
RT "Evaluation of Receptor Tyrosine Kinase Expression in Canine Brain  
Tumors";  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Mallen-StClair J., London C.A.;  
RT "The Role of PDGFR in Canine Cancer";  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
CC 1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC 1- SIMILARITY: Belongs to the Tyr family of protein kinases. CSP-  
1/PDGF receptor subfamily.  
CC EMBL; AY25124; AAS91495.2; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.  
DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR007119; Prot\_kinase.  
DR InterPro; IPR001824; RecepttyrkinaseIII.  
DR InterPro; IPR002290; Ser thr pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
DR InterPro; IPR009134; VEGFR.  
DR Pfam; PF00047; Ig; 2.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR01832; VEGFRECEPTOR.  
DR ProDom; PD000001; Prot\_kinase; 2.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00408; IGC2; 3.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; TYRG; 1.  
DR PROSITE; PS50835; IG Like; 2.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;  
KW Phosphorylation; Receptor; Transferase; Transmembrane.  
FT NON\_TER 1  
SQ SEQUENCE 1079 AA; 121934 MW; 3DA424B9C1339D6B CRC64;

Query Match 95.5%; Score 5400; DB 2; Length 1079;  
Best Local Similarity 95.9%; Pred. No. 2.2e-283;  
Matches 1035; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY 11 LGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSRLCRGSESEVSNQYPMEESDVE 70  
Db 1 LGCLLAGPSLILCOLSLPSILPNEKVKVQLNSSFSRLCRGSESEVSNQYPMEESDVE 60

QY 71 IRNEENNSGLFVTVLEVSASAAHTGLYTCYNNHTQTEENLEGRHIIYVPPDPAFVP 130  
 Db 61 IRNEENNSGLFVTVLEVNASAAHTGLYTCYNNHTQTEENLEGRHIIYVPPDPAFVP 120  
 QY 131 LGMTDYLIVEDDDSAIICRTTDPETPTVLNSGVVPASDSRQGFNGTFTVGPYICE 190  
 Db 121 LGMTDYLIVEDDDSAIICRTTDPETPTVLNSGVVPASDSRQGFNGTFTVGPYICE 180  
 QY 191 ATVKGKGFOTIPPNVYALKATSELDLEALATVVKSGETIVVTCVAFNNEVVDLQWTV 250  
 Db 181 ATVKGKGFOTIPPNVYALKATSELDLEALATVVKSGETIVVTCVAFNNEVVDLQWTV 240  
 QY 251 GEVKGKGIITLBEIKVPSIKLYTVTTVPATVKDSGYECAARQATREYKEMKKVTISVH 310  
 Db 241 GEVKGKGIITLBEIKVPSIKLYTVTTVPATVKDSGYECAARQATREYKEMKKVTISVH 300  
 QY 311 EKGFTIEKPTFQLEAVNLHVKHFVVEVRAVPPRISWLNKLNLTLENLTITTDVEKI 370  
 Db 301 EKGFTIEKPTFQLEAVNLHVKHFVVEVRAVPPRISWLNKLNLTLENLTITTDVEKI 360  
 QY 371 QEIRVRSKLLIRAKEEDSGHTIIVAOEDAVKSYTFELLTQVPSILDLVDDHGGSTG 430  
 Db 361 QEIRVRSKLLIRAKEEDSGHTIIVAOEDAVKSYTFELLTQVPSILDLVDDHGGSTG 420  
 QY 431 QTVRCTAECTPLPDIEWMICKDKKCNNETSWTILANNVSNITTEIHSRDRSTVEGRVTF 490  
 Db 421 QTVRCTAECTPLPDIEWMICKDKKCNNETSWTILANNVSNITTEIHSRDRSTVEGRVTF 480  
 QY 491 AKVEETIARCLAKNLLGHENRELKLVAPTLSELTVAAAVLVLLVIVIVISLVLVWIK 550  
 Db 481 TRVEETIARCLAKNLLGHENRELKLVAPTLSELTVAAAVLVLLVIVIVISLVLVWIK 540  
 QY 551 QKPRYBIRNRVLESIPDGEHYIYVDPMLPVDSEWFFPDGLVGRVLGSGAFGVKVBG 610  
 Db 541 QKPRYBIRNRVLESIPDGEHYIYVDPMLPVDSEWFFPDGLVGRVLGSGAFGVKVBG 600  
 QY 611 TAYGLSRQFVNMKAVKMLKPTARSEKQALMSKIMTHLPHLNLVLLGACTKSGPI 670  
 Db 601 TAYGLSRQFVNMKAVKMLKPTARSEKQALMSKIMTHLPHLNLVLLGACTKSGPI 660  
 QY 671 YIITEYCFYGLDVLNHLKRDSEFLSHHPKPKKELDIFGLNPADESTRSYVILSPENNGD 730  
 Db 661 YIITEYCFYGLDVLNHLKRDSEFLSHHPKPKKELDIFGLNPADESTRSYVILSPENNGD 720  
 QY 731 YNDMKQADTQVVPMLERKEVSKYSDIQSLYDRPASYYKKSMLESEVKNLLSDDNSGL 790  
 Db 721 YNDMKQADTQVVPMLERKEVSKYSDIQSLYDRPASYYKKSMLESEVKNLLSDDNSGL 780  
 QY 791 TLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLARDIMHDSNTV 850  
 Db 781 TLDDLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLARDIMHDSNTV 840  
 QY 851 SKGSTFLPKWMAPEIFDNLVLTSLSDVMSYGLLWEIFSLGTPYPCGMVDSFTFNKIK 910  
 Db 841 SKGSTFLPKWMAPEIFDNLVLTSLSDVMSYGLLWEIFSLGTPYPCGMVDSFTFNKIK 900  
 QY 911 SGYRMAKPDHATSEVVEIWMKCNSEPKRPSFYHLSEIVENLLPQYKYSYKIKHLDFL 970  
 Db 901 SGYRMAKPDHATSEVVEIWMKCNSEPKRPSFYHLSEIVENLLPQYKYSYKIKHLDFL 960  
 QY 971 KSDHPAVARMVDSNAYIGVTYKNEEDKLKOWEGGLDEQRLSADSGYIIPLPIDPVPPE 1030  
 Db 961 KSDHPAVARMVDSNAYIGVTYKNEEDKLKOWEGGLDEQRLSADSGYIIPLPIDPVPPE 1020  
 QY 1031 EEDLGRNHSSTQSESAIETGSSSSTFKREDETIEDIMDDDIIGIDSSDLVEDSFL 1089  
 Db 1021 EEDLGRNHSSTQSESAIETGSSSSTFKREDETIEDIMDDDIIGIDSSDLVEDSFL 1079

RESULT 3

Q7TSJ3

ID Q7TSJ3

AC Q7TSJ3

PRELIMINARY; PRT; 1089 AA.

DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE pdgfra protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=23888257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-  
 CC 1/PDGF receptor subfamily.  
 DR EMBL; BC053036; AAH53036.1; --  
 DR HSSP; P36888; 1RBJ.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR GO; GO:0030539; P:male genital morphogenesis; IMP.  
 DR GO; GO:0009887; P:organogenesis; IMP.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_C2.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001824; RecepttyrkinIII.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR Pfam; PF00047; igf\_2.  
 DR ProDom; PD000001; Prot\_kinase; 2.  
 DR SMART; SM00408; IGC2; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
 DR ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;  
 KW Phosphorylation; Receptor; Transferase; Transmembrane;  
 KW Tyrosine-protein kinase.  
 SQ SEQUENCE 1089 AA; 122682 MW; 07AAPFD2AA12533A CRC64;

Query Match 92.6%; Score 5232; DB 2; Length 1089;

Best Local Similarity 91.8%; Pred. No. 2.7e-274;

Matches 1000; Conservative 48; Mismatches 41; Indels 0; Gaps 0;

QY 1 MGTSHPAFLVGLGLTGLSLILCOLSLPSILNENKVVQLNSSFSLRCFGESEVSWQYP 60

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Db 1 MGTSHQVFLVLSCLTGPGLISCOLLPSILPNEKIVQLNSSFSLRCVGESEVSWQHP 60
QY 61 MSBEESDVIRNEENNSGLFVTVLEVSSASAHTGLTYCYNHNTOTEEENLEGRHIYY 120
Db 61 MSEDPPNVEIRSEENNSGLFVTVLEVSSASAHTGWTCYNYHTQDSEIEGRHIYY 120
QY 121 VPDPDAFVPLGMDYLVIVVEDDSAIIPCRTPDPPTVTLHNSGVVPASYSRQGFNG 180
Db 121 VPDPDAFVPLGMDYLVIVVEDDSAIIPCRTPDPPTVTLHNSGVVPASYSRQGFNG 180
QY 181 TPTVGVYICBATYKGGKFTQIPNVYALKATSELDLEMEALKTVYKSGETIVVTCVFN 240
Db 181 TFSVGVYICBATYKGGKFTQIPNVYALKATSELDLEMEALKTVYKSGETIVVTCVFN 240
QY 241 EVVDLQWTPYGEVKGITMLEIKVPSIKLVTLTVPEATVKDSDGYECAAQAQREV 300
Db 241 EVVDLQWTPYGEVKGITMLEIKVPSIKLVTLTVPEATVKDSDGYECAAQAQREV 300
QY 301 EMKQVTSVHEKGFIEIKPTFSQLEAVNLHVKHFVVEVRAVPPPRISMLKNNLTLE 360
Db 301 EMKRVTSVHEKGFVIEPTFGQLEAVNLHVEFVVEVQAYPTPRISMLKNNLTLE 360
QY 361 TEITTDVEKIQETRYSKLIRAKEDSDHYTIVAQNEADVKSFTFELLTQVPSILD 420
Db 361 TEITTDVQKSOETRYOSKLIIRAKEDSDHYTIIQNEEDVKSFTFELLTQVPSILD 420
QY 421 VDDHGSQTGQVRCVTAEGTFLPDIEWMICKDKCNETSWTILANNVSNITETHSRD 480
Db 421 VDDHGSQGTQVRCVTAEGTFLPDIEWMICKDKCNETSWTILANNVSNITETLPRG 480
QY 481 RSTVEGRVTFPAKVEETIAVCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLV 540
Db 481 RSTVEGRVTFPAKVEETIAVCLAKNLLVARELKVAPTLRSELTVAAAVLVLLV 540
QY 541 SLILVVIWKQKPRYIRWRVIESISPDGHEYIYVDPQMQLPYDSRNEFPDGLVLR 600
Db 541 SLILVVIWKQKPRYIRWRVIESISPDGHEYIYVDPQMQLPYDSRNEFPDGLVLR 600
QY 601 SGAFKVVGTAYGLRSQVPMKAVKMLKPTARSSEKQALMSSELKIMTHLGPLH 660
Db 601 SGAFKVVGTAYGLRSQVPMKAVKMLKPTARSSEKQALMSSELKIMTHLGPLH 660
QY 661 LGACTKSGPIYITTECFYGDLYNLHKNRDSFLSHPEKPKKELDI FGLNPADESTR 720
Db 661 LGACTKSGPIYITTECFYGDLYNLHKNRDSFMSQHPKPKKLDI FGLNPADESTR 720
QY 721 VILSPENGDYMDKQADTTQYVPMLEKEVSKYDIQSLYDRPASYKKKSLMDSEVK 780
Db 721 VILSPENGDYMDKQADTTQYVPMLEKEVSKYDIQSLYDRPASYKKKSLMDSEVK 780
QY 781 LLSDDNSEGLTLLDLASFYQVARGMEFLASKNCVHRDLAARNVLLAQKIVKICD 840
Db 781 LLSDDNSEGLTLLDLASFYQVARGMEFLASKNCVHRDLAARNVLLAQKIVKICD 840
QY 841 RDIMHDSNVYKSGSTPLPKWMAPEGIFDNLYTTLSDVMSYGLLWEIFSLGCTPP 900
Db 841 RDIMHDSNVYKSGSTPLPKWMAPEGIFDNLYTTLSDVMSYGLLWEIFSLGCTPP 900
QY 901 VDSFTFNKIKSGYRMKAPDHATSEVYEMVCKWNSPEKRPSPYHLSEIVENLLPQ 960
Db 901 VDSFTFNKIKSGYRMKAPDHATSEVYEMVCKWNSPEKRPSPYHLSEIVENLLPQ 960
QY 961 SYEKIHLDFLKSHPAVARVDSNAYIGVTYKNEEDKLKOWEGGLDQRLSADSGY 1020
Db 961 SYEKIHLDFLKSHPAVARVDSNAYIGVTYKNEEDKLKOWEGGLDQRLSADSGY 1020
QY 1021 PLPDDIPVPEEDLGRNHRSSQTSBESAIETGSSSSTFKREDETIEDIMDDIG 1080
Db 1021 PLPDDIPVPEEDLGRNHRSSQTSBESAIETGSSSSTFKREDETIEDIMDDIG 1080
QY 1081 SLDVEDSFL 1089
Db 1081 SLDVEDSFL 1089
```

RESULT 4  
PGDS\_MOUSE STANDARD; PRT; 1089 AA.  
AC P26618; Q62046;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112) (PDGF-R-alpha).  
DE Name=PDGFra;  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=91061789; PubMed=2174116;  
RA Stiles C.D., Wang C.;  
RT "Retinoic acid promotes transcription of the platelet-derived growth factor alpha-receptor gene";  
RL Mol. Cell. Biol. 10:6781-6784(1990).  
RN [2]  
SEQUENCE FROM N.A.  
RX MEDLINE=92334866; PubMed=1321404;  
RA Do M.S., Fitzer-Attas C., Gubbay J., Greenfield L., Feldman M., Eisenbach L.;  
RT "Mouse platelet-derived growth factor alpha receptor: sequence, tissue-specific expression and correlation with metastatic phenotype";  
RL Oncogene 7:1567-1575(1992).  
CC -!- FUNCTION: Receptor that binds both PDGFA and PDGFB and has a tyrosine-protein kinase activity.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.  
CC -!- SUBUNIT: Homodimer, and heterodimer with PDGFRB.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSP-1/PDGF receptor subfamily.  
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL; M84607; AAA39904.1; -;  
CC EMBL; M57683; AAA39733.1; -;  
CC PIR; I57511; S33727.  
CC HSP; P11362; 1FGK.  
CC MGD; MGI:97530; Pdgfra.  
CC GO; GO:0030539; P: male genital morphogenesis; IMP.  
CC GO; GO:0009887; P: organogenesis; IMP.  
CC InterPro; IPR007110; IG-like.  
CC InterPro; IPR003598; IG\_c2.  
CC InterPro; IPR011009; Kinase like.  
CC InterPro; IPR000719; Prot kinase.  
CC InterPro; IPR001824; RecepttyrkinasII.  
CC InterPro; IPR001245; Tyr\_kinase.  
CC InterPro; IPR008266; Tyr\_kinase\_AS.  
CC InterPro; IPR009134; VEGFR.  
CC Pfam; PF00047; ig; 4.  
CC PRINTS; PR01832; VEGFRECEPTOR.  
CC ProDom; PD000001; Prot kinase; 2.  
CC SMART; SM00408; IGC2; 1.  
CC SMART; SM00219; Tyrc; 1.  
CC PROSITE; PS00835; IG\_LIKE; 3.  
CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_LIII; 1.  
 KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;  
 KW Receptor; Repeat; Signal; Transferase; Transmembrane;  
 KW Tyrosine-protein kinase.  
 FT SIGNAL 1 24 Potential.  
 FT CHAIN 25 1089 Alpha platelet-derived growth factor receptor.  
 FT DOMAIN 25 525 Extracellular (Potential).  
 FT TRANSMEM 526 549 Potential.  
 FT DOMAIN 550 1089 Cytoplasmic (Potential).  
 FT DOMAIN 25 113 Ig-like C2-type 1.  
 FT DOMAIN 214 306 Ig-like C2-type 3.  
 FT DOMAIN 319 410 Ig-like C2-type 4.  
 FT DOMAIN 593 954 Protein kinase.  
 FT NP\_BIND 599 607 ATP (By similarity).  
 FT BINDING 627 677 ATP (By similarity).  
 FT ACT\_SITE 818 818 By similarity.  
 FT CARBOHYD 42 42 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 76 76 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 89 89 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 103 103 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 179 179 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 353 353 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 359 359 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 458 458 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 468 468 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 506 506 N-linked (GlcNAc... ) (Potential).  
 FT CONFLICT 192 192 T -> A (in Ref. 1).  
 FT CONFLICT 202 202 E -> A (in Ref. 1).  
 FT CONFLICT 252 252 E -> G (in Ref. 1).  
 FT CONFLICT 271 271 L -> V (in Ref. 1).  
 FT CONFLICT 322 322 G -> S (in Ref. 1).  
 FT CONFLICT 326 326 A -> P (in Ref. 1).  
 FT CONFLICT 439 440 GT -> EG (in Ref. 1).  
 FT CONFLICT 529 529 A -> E (in Ref. 1).  
 FT CONFLICT 737 737 A -> D (in Ref. 1).  
 FT CONFLICT 849 849 Y -> D (in Ref. 1).  
 FT CONFLICT 936 936 E -> D (in Ref. 1).  
 FT CONFLICT 950 950 V -> L (in Ref. 1).  
 FT CONFLICT 1005 1005 S -> G (in Ref. 1).  
 SQ SEQUENCE 1089 AA; 122727 MW; B3A3B246716249E0 CRC64;  
 Query Match 92.5%; Score 5229; DB 1; Length 1089;  
 Best Local Similarity 91.8%; Pred. No. 4e-274;  
 Matches 1000; Conservative 47; Mismatches 42; Indels 0; Gaps 0;  
 QY 1 MGTSHPAFLVGLCLTGLSLILCOLSLPILPNEKVKVQLNSSFSLRCFGESEVSWQYP 60  
 DB 1 MGTSHQVFLVSLCLLTGPGGLISQQLLPILPNEKEIKVQLNSSFSLRCVGESEVSWQHP 60  
 QY 61 MSSEESDVEIRNEENNSGLFVTVLEVSSASAAHTGLTYCYNHTQTENELEGRHIYY 120  
 DB 61 MSSEEDPNVEIRSEENNSGLFVTVLEVSNASAAHTGTYCYNHTQTDESEIEGRHIYY 120  
 QY 121 VPDPDAFVPLGMDVLIIVVEDDSALIPCRITDPTPTVTLHNSGVPPASVDSROGNG 180  
 DB 121 VPDPDAFVPLGMDVLIIVVEDDSALIPCRITDPTPTVTLHNSGRVLPASVDSROGNG 180  
 QY 181 TFTVGYICEATYKGGKFQIPENVYALKATSELDLEMEALKTIVYKSGETIVVTCVFN 240  
 DB 181 TFSVGPVCEATYKGRFTKTFSENVYALKATSELNLEMDARQIVYKAGETIVVTCVFN 240  
 QY 241 EVVDLQWTPGEVKGKGTIMLEIKVPSIKLVTVLTPVPEATVDSGDYECARQATREV 300  
 DB 241 EVVDLQWTPGEVNRKGTIMLEIKVPSIKLVTVLTPVPEATVDSGDYECARQATREV 300  
 QY 301 EMKVTISVHEKGFIEIKTPFSOLEAVNLHVKHVVVVRVAYPPPRISWLNKNTLIENL 360  
 DB 301 EMKRVISVHEKGFVEIEPTFGQLEAVNLHVEVFEVVEVQAYPTPRISWLNKNTLIENL 360  
 QY 361 TEITTDVEKIQEIRYRSKLLIRAKEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 420

DB 361 TEITTDVQKQSTRYQSKLLIRAKEDSGHYTIVQNEEDVKSXYTFELSLVPAISILD 420  
 QY 421 VDDHGGSTGGQVRCVCTAGTPTLPDIEMWICKDKKCNNTSWTILANNVSNITTEHSRD 480  
 DB 421 VDDHGGSGGQVRCVCTAGTPTLPDIEMWICKDKKCNNTSWTILANNVSNITTEHSRD 480  
 QY 481 RSTVEGRVTFKVEETIAVRCIAKLLGAENRELKIVAPTLRSELTVAAAVLVLLVIV 540  
 DB 481 RSTVEGRVTFKVEETIAVRCIAKLLGAENRELKIVAPTLRSELTVAAAVLVLLVIV 540  
 QY 541 SLIVLVVIMKQKPRYBIRWRVIESIPDGHGHEIYVDPMLQPYDSRWEFFPRDGLVGLRG 600  
 DB 541 SLIVLVVIMKQKPRYBIRWRVIESIPDGHGHEIYVDPMLQPYDSRWEFFPRDGLVGLRG 600  
 QY 601 SGAFKVVGEVGTAYGLSRSPVPMKVAVKMLKPTARSEKQALMSSELKIMTHLGHNLVNL 660  
 DB 601 SGAFKVVGEVGTAYGLSRSPVPMKVAVKMLKPTARSEKQALMSSELKIMTHLGHNLVNL 660  
 QY 661 LGACTKSGPIIYITEYCFYGDVLYLHKNRDSFLSHHPEKPKKELDI FGLNPADESTSY 720  
 DB 661 LGACTKSGPIIYITEYCFYGDVLYLHKNRDSFLSHHPEKPKKELDI FGLNPADESTSY 720  
 QY 721 VILSFENNGDYMDKQADTTQVPMLEKEVSKYDIQISLYDRPASYYKKKSMLDSEVK 780  
 DB 721 VILSFENNGDYMDKQADTTQVPMLEKEVSKYDIQISLYDRPASYYKKKSMLDSEVK 780  
 QY 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCHVDRDLAARNVLLAOKIKVICDFGLA 840  
 DB 781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCHVDRDLAARNVLLAOKIKVICDFGLA 840  
 QY 841 RDIMHDSNVYKSGTFLPVKNWAPESIFDNLYTLTSDVMSYGILLWEIFSLGCTPPGM 900  
 DB 841 RDIMHDSNVYKSGTFLPVKNWAPESIFDNLYTLTSDVMSYGILLWEIFSLGCTPPGM 900  
 QY 901 VDSTFYNKIKSGYRMKPDHATSEVVEIMVKNWSEPEKRPSPFYLSEIVENLLPQYKK 960  
 DB 901 VDSTFYNKIKSGYRMKPDHATSEVVEIMVKNWSEPEKRPSPFYLSEIVENLLPQYKK 960  
 QY 961 SYEKIHLDFLKDHPAARMVDSNAYIGVTKNEEDKLDKQWEGGLDQRLSADSGYII 1020  
 DB 961 SYEKIHLDFLKDHPAARMVDSNAYIGVTKNEEDKLDKQWEGGLDQRLSADSGYII 1020  
 QY 1021 PLPDIIDPVEEEDLGRNHSQTSSESATETGSSSTFIKREDETIEDIMDDIGIDS 1080  
 DB 1021 PLPDIIDPVEEEDLGRNHSQTSSESATETGSSSTFIKREDETIEDIMDDIGIDS 1080  
 QY 1081 SOLVEDSFL 1089  
 DB 1081 SOLVEDSFL 1089  
 RESULT 5  
 PGDS\_RAT  
 ID PGDS\_RAT STANDARD; PRT; 1088 AA.  
 AC P20786;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112) (PDGF-R-alpha).  
 GN Name=PDGfra;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=90220609; PubMed=2157969;  
 RA Lee K.H., Bowen-Pope D.F., Reed R.R.;  
 RT Isolation and characterization of the alpha platelet-derived growth factor receptor from rat olfactory epithelium.";



RL Mol. Cell. Biol. 10:2237-2246(1990).  
 RN [2]  
 RP SEQUENCE OF 33-524 FROM N.A.  
 RX MEDLINE=93305723; PubMed=8318539; DOI=10.1016/0167-4781(93)90127-Y;  
 RA Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;  
 RT "Conservation in sequence and affinity of human and rodent PDGF  
 RT ligands and receptors.";  
 RL Biochim. Biophys. Acta 1173:294-302(1993).  
 CC -!- FUNCTION: Receptor that binds both PDGFA and PDGFB and has a  
 CC tyrosine-protein kinase activity.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBUNIT: Homodimer, and heterodimer with PDGFRB.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGFR  
 CC receptor subfamily.  
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC -----  
 DR EMBL; M63837; AAA40743.1; ALT\_INIT.  
 DR EMBL; Z14118; CAA78488.1; -.  
 DR PIR; A34710; PERTGA.  
 DR HSSP; P11362; IFGX.  
 DR RGD; 3284; Pdgfra.  
 DR InterPro; IPRO03599; Ig.  
 DR InterPro; IPRO07110; Ig-like.  
 DR InterPro; IPRO11009; Kinase like.  
 DR InterPro; IPRO00719; Prot kinase.  
 DR InterPro; IPRO01824; RecepttyrkinIII.  
 DR InterPro; IPRO01245; Tyr\_pkinase.  
 DR InterPro; IPRO08266; Tyr\_pkinase\_AS.  
 DR InterPro; IPRO09134; VEGFR.  
 DR Pfam; PF00047; Ig; 4.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR01832; VEGFRECEPTOR.  
 DR ProDom; PD000001; Prot\_kinase; 2.  
 DR SMART; SM00409; IG; 3.  
 DR SMART; SM00219; TyrKC; 1.  
 DR PROSITE; PS00835; IG LIKE; 3.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
 KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;  
 KW Receptor; Repeat; Signal; Transferase; Transmembrane;  
 KW Tyrosine-protein kinase.  
 FT SIGNAL 1 23  
 FT CHAIN 24 1088 Alpha platelet-derived growth factor  
 FT receptor.  
 FT DOMAIN 24 524 Extracellular (Potential).  
 FT TRANSMEM 525 548 Potential.  
 FT DOMAIN 549 1088 Cytoplasmic (Potential).  
 FT DOMAIN 25 112 Ig-like C2-type 1.  
 FT DOMAIN 213 305 Ig-like C2-type 3.  
 FT DOMAIN 318 409 Ig-like C2-type 4.  
 FT DOMAIN 592 953 Protein kinase.  
 FT NP\_BIND 598 606 ATP (By similarity).  
 FT BINDING 626 626 ATP (By similarity).  
 FT ACT\_SITE 817 817 By similarity.  
 FT MOD\_RES 848 848 Phosphotyrosine (by autocatalysis) (By  
 FT similarity).  
 FT CARBOHYD 41 41 O-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 75 75 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 102 102 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 178 178 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 352 352 N-linked (GlcNAc... ) (Potential).

FT	CARBOHYD	358	358	N-linked (GlcNAc... ) (Potential).
FT	CARBOHYD	457	457	N-linked (GlcNAc... ) (Potential).
FT	CARBOHYD	467	467	N-linked (GlcNAc... ) (Potential).
FT	CONFLICT	150	150	L -> R (in Ref. 2).
FT	CONFLICT	519	519	S -> T (in Ref. 2).
SQ	SEQUENCE	1088	AA; 122641	MM; 590C8BB0418801E7 CRC64;

Query Match 91.8%; Score 5190.5; DB 1; Length 1088;  
 Best Local Similarity 90.9%; Pred. No. 4.8e-272;  
 Matches 990; Conservative 55; Mismatches 43; Indels 1; Gaps 1;

QY	1	MCTSHPAFLVLCGLTGLSLILCOLSLPSLPLNENEKVLQNSFSLSRCFGESEVSNQYP	60
DB	1	MGTSQ-AFVLSCLLTGPLSLVLCQLLPSLPLNENEKIVPLSSFSLSRCFGESEVSNQHP	59
QY	61	MSSESDSEIRNEENNSGLFTVLEVSASAAHTGLTYCYNHTQTETNELEGRHIYY	120
DB	60	MSEEDPNVEIRTEENSSLFVTLEVNASAAHTGWTYCYNHTQTETNELEGRHIYY	119
QY	121	VDPDVAFLVPLGMDTYLVIVEDDDSAIIPCTRTDPTPTVLHNSGVVPASYSRQGFNG	180
DB	120	VDPDVAFLVPLGMDTYLVIVEDDDSAIIPCLATDPTPTVLHNSGRVLPASYSRQGFNG	179
QY	181	TFTVGPYICATYKGGKFTIPNYYALKATSELDLEMEALKTVYKSGETIVVTCVFN	240
DB	180	TFSVGPYICATYVGRGTRFKTSFNYYALKATSELNLEMDTRQTVYKAGETIVVTCVFN	239
QY	241	EVDVLQWTPYGEVKGKIGITMELBEIKVPSIKLVYTLVPEATVKDSDGYECAAQAQREV	300
DB	240	EVDVLQWTPYGEVKNKIGITMELBEIKVPSIKLVYTLVPEATVKDSDGYECAAQAQREV	299
QY	301	EMKVTISVHEKGFIEIKFTFQSLQEAVALNHEVHFVVEVRAVPPPRISMKNLTIENL	360
DB	300	EMKVTISVHEKGFVQIRPTFGHLETNVLHQVREFVVEVQAVPTPRISMKNLTIENL	359
QY	361	TRITTVVEKIOEIRYPSKLIIRAKEEDSGHTYIVQNEADAVKSYTFELLTQVPSLTL	420
DB	360	TEITTVQSRQETRYQSKLIIRAKEEDSGHTYIVQNDMDKSYTFELSTLPASILEL	419
QY	421	VDDHGGSTGGQVRCVTAEGTPLDIEWMI CKDKCNETSWTILANNYSNIITEHSRD	480
DB	420	VDDHGGSGGQVRCVTAEGTPLDIEWMI CKDKCNETSWTILANNYSNIITEHQRG	479
QY	481	RSTVEGRVTFPAKVEETIAVRCIAKLLGAENRELKLVAPLRSLETVAALVLLVIVII	540
DB	480	RSTVEGRVTFPAKVEETIAVRCIAKLLGAENRELKLVAPLRSLETVAALVLLVIVII	539
QY	541	SLIVLVIWKQKPRYIRWRVIESIPDGHEYIYVDPMLPYDSRWEFFRDGLVGLG	600
DB	540	SLIVLVIWKQKPRYIRWRVIESIPDGHEYIYVDPMLPYDSRWEFFRDGLVGLG	599
QY	601	SGAFKGVGVTAGLSRSOPVMKVAVKMLKPTARSSEKQALMSSELKIMTHLGPLHINVL	660
DB	600	SGAFKGVGVTAGLSRSOPVMKVAVKMLKPTARSSEKQALMSSELKIMTHLGPLHINVL	659
QY	661	LGACTKSGPIYITTEYCFYGDVLYNLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY	720
DB	660	LGACTKSGPIYITTEYCFYGDVLYNLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSY	719
QY	721	VILSPENNGDYMDKQADTTQVVPMLERKEVSKYSIQISLYDRPASYSKKKSLMDESKN	780
DB	720	VILSPENNGDYMDKQADTTQVVPMLERKEVSKYSIQISLYDRPASYSKKKSLMDESKN	779
QY	781	LISDONSSEGLTLLDLLSFTYQVARGMEFLASKNCHVRDLAARNVLLAQGKIVKICDFGLA	840
DB	780	LISDONSSEGLTLLDLLSFTYQVARGMEFLASKNCHVRDLAARNVLLAQGKIVKICDFGLA	839
QY	841	RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGLLWEIFSLGCTPYPGMM	900
DB	840	RDIMHDSNVYKSGSTFLPVKWMAPESIFDNLYTTLSDVMSYGLLWEIFSLGCTPYPGMM	899
QY	901	VDSTFVNKIKSGYRMAKPHATSEVVEIMVKNSEPEKPSFYHLSEIVENLLPGQYKK	960

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Db 900 VDSFTYKIKSGYRMKAPDHATSEVYEMVQWNSSEPKRPSFYHLSEIVENLLPQYKK 959
Qy 961 SYEKIHLDFKSDHPAVARVDSNAYIGVTVKNEEDKLDWEGGLDEQRLSADSGYII 1020
Db 960 SYEKIHLDFKSDHPAVARVDSNAYIGVTVKNEEDKLDWEGGLDEQRLSADSGYII 1019
Qy 1021 PLPDDIPVEEEDLGRNHRSSQTSSESALETGSSSSTFKRDETIEDIDMMDDIGIDS 1080
Db 1020 PLPDDIPVEEEDLGRNHRSSQTSSESALETGSSSSTFKRDETIEDIDMMDDIGIDS 1079
Qy 1081 SOLVEDSFL 1089
Db 1080 SOLVEDSFL 1088

RESULT 6
ID Q9PUF6 PRELIMINARY; PRT; 1087 AA.
AC Q9PUF6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Platelet-derived growth factor receptor alpha.
GN Name=PDGFR- $\alpha$ ;
OS Gallus Gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2032546; PubMed=10842055; DOI=10.1016/S0925-4773(00)00321-X;
RA Atalotia P.;
RT "Platelet-derived growth factor A modulates limb chondrogenesis both in vivo and in vitro.";
RL Mech. Dev. 94:13-24(2000).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSP-1/PDGF receptor subfamily.
CC EMBL: AF188842; AAF01460.1; -.
DR HSSP; P36888; 1RJB.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 1087 AA; 122939 MW; F3306BDD3D983E31 CRC64;

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Query Match 81.0%; Score 4577; DB 2; Length 1087;
Best Local Similarity 80.3%; Pred. No. 7,1e-239;
Matches 875; Conservative 95; Mismatches 116; Indels 4; Gaps 4;

Qy 1 MGTSHAPFLVIGCLLTGLSLILCOLSLPSILPNEKVVQLNSPFLRCFCGSESEVSWQYP 60
Db 1 MGTTPRTFLILGCLTGLPLLTLCQLPLEFTVFNRMVQLNSFTLKCGSDSEVSWQYP 60
Qy 61 MSEESESSDVEIENEENNSGLFVTVLEVSASAAHGLTYCYNHTQTENELEGRHIYIY 120
Db 61 VT-EGSHRIDIRHEENNSGLFVTVLEGNASAAHGMVVCYNNHTQVEDGEVEGKDIYIY 119
Qy 121 VPDPDVAFVPLGWTDLVIVEDDDSAIIPCRITTPETPTVLHNS-EGVVPASYSRQGFN 179
Db 120 VPDPMFVPSLPEDQFILVEESGDPVPIPCRTSDPSAEVTLVNSLDKPVYAFVDSKQGFV 179
Qy 180 GTFTVGPICEATYVGKQFQTIPFNYYALKATSELDLEMEALKTVYKSEITIVTCAVEN 239
Db 180 GNFLAGPYCTKTWVGVEFKSDEFILYILRATSQLPVEIALKTVYKGETIIVTCCVFD 239
Qy 240 NEVVDLQWTPGCEVKGKGTMLKEIKVPSIKLAVYTLTVPEATVKDSGDYECARQATREV 299
Db 240 NEVNLQWNPQKVKREKGLIKUDDIKVPSQKLVYMLTTPDVLVKDTGDIECTARHATKEV 299
Qy 300 KEMKVTISVHEKGFIEIKPTFSQLEAVNLHEVHFVVEVRAYPPIRISWLKKNLTLIEN 359
Db 300 KENKKVITVHDKGFHLEFPQSPLEAVNLHEVKNFVVDVQVAPAPKMYLAKDNVTLIEN 359
Qy 360 LTEITTDVEKIOEIRYRKLKLIIRAKEEDSGHYTIVAQNEADVSKSYTFELLTQVSSILD 419
Db 360 LTEIVTSSNRVQETRFQSKLIRAKEEDSGTILMLLKNEDEIKRYTFSELLIQVPALILD 419
Qy 420 LVDDHSGTGGGTCTAEGTPLDIEWMI CKDIKKCNNETSWTILANNVSNIIITEIHR 479
Db 420 LMDDHQSAGRTVRCLAGTEPLDVEVLVCKDIKKCSNDTSTWTLTNNISDIHMEALD 479
Qy 480 DRSTVEGRVTFKVBETIAVRCLAKNLGAENRELKLVAPTIRSELTVAAAVLVLLVVI 539
Db 480 ERNVESQVTPQKVEETLAVRCVARNDLGAVTRELLKLVAPTIRSELTVAAAVLVLLVVI 539
Qy 540 ISLIVLVVWKKOPRYEIRWRVIESISPDGHEYIYVDPNOLPYDSRWEPRGLVGLV 599
Db 540 ISLIVLVVWKKOPRYEIRWRVIESISPDGHEYIYVDPNOLPYDSRWEPRGLVGLV 599
Qy 600 GSGAFKGVVEGTAYGLSRQPVKAVKMLKPTASRSEKQALMSELKINTHGLPHLNIYN 659
Db 600 GSGAFKGVVEGTAYGLSRQPVKAVKMLKPTASRSEKQALMSELKINTHGLPHLNIYN 659
Qy 660 LLGACTKSGPIYIITEYCFYDGLVNYLHKRDSFSLSHPEKPKKELDIFGLNPADESTRS 719
Db 660 LLGACTKSGPIYIITEYCFYDGLVNYLHKRDNFSLSRHPEKPKKOLDIFGMNPADESTRS 719
Qy 720 YVILSPENNGDYMDKQADTTOYVPMLEKEYSKYSIDORSLYDRPASVKKSMLDSEVK 779
Db 720 YVILSPENNGDYMDKQADTTOYVPMLEKEYSKYSIDORSLYDRPASVKKSMLDSEVK 779
Qy 780 NLLSDNNSGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOCKIVKICDFGL 839
Db 780 NLLSDNNSGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOCKIVKICDFGL 839
Qy 840 ARDIMHDSNYVSKGSTFLPVKMWAPESIFDNLVYTLSDVMSYGILLWEIFSLGGTYPGM 899
Db 840 ARDIMHDSNYVSKGSTFLPVKMWAPESIFDNLVYTLSDVMSYGILLWEIFSLGGTYPGM 899
Qy 900 MVDSTFYNKIKSGYRMKAPDHATSEVYEMVQWNSSEPKRPSFYHLSEIVENLLPQYK 959
Db 900 MVDSTFYNKIKSGYRMKAPDHATSEVYEMVQWNSSEPKRPSFYHLSEIVENLLPQYK 959
Qy 960 KSYEKIHLDFKSDHPAVARVDSNAYIGVTVKNEEDKLDWEGGLDEQRLSADSGYI 1019
Db 960 KSYEKIHLDFKSDHPAVARVDSNAYIGVTVKNEEDKLDWEGGLDEQRLSADSGYI 1018
Qy 1020 IPLFDIDPVPEBEDLGRNHRSSQTSSESALETGSSSSTFKRDETIEDIDMMDDIGID 1079

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Db	1019	TLPLDPIDPVESEDE-LGKRNRHSSQTSSESAIETGSSSTFKREDETIEDIMDDIGID	1077
Qy	1080	SSDLVEDSFL 1089	
Db	1078	SSDLVEDSFL 1087	
RESULT 7			
PGDS XENLA			
ID	PGDS XENLA	STANDARD;	PRT; 1087 AA.
AC	P26619;		
DT	01-AUG-1992	(Rel. 23, Created)	
DT	01-AUG-1992	(Rel. 23, Last sequence update)	
DT	05-JUL-2004	(Rel. 44, Last annotation update)	
DE	Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112)		
DE	(PDGF-R-alpha).		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=93365089; PubMed=9358864;		
RX	Jones S.D., Ho L., Smith J.C., Yordan C., Stiles C.D., Mercola M.;		
RA	"The Xenopus platelet-derived growth factor alpha receptor: cDNA		
RT	cloning and demonstration that mesoderm induction establishes the		
RT	lineage-specific pattern of ligand and receptor gene expression."		
RL	Dev. Genet. 14:185-193(1993).		
CC	-!- FUNCTION: Receptor that binds both PDGFA and PDGFB and has a		
CC	tyrosine-protein kinase activity.		
CC	-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein		
CC	tyrosine phosphate.		
CC	-!- SUBUNIT: Homodimer, and heterodimer with PDGFRB.		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF		
CC	receptor subfamily.		
CC	-!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ).		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .		
CC	EMBL; M80798; AAA49929.1; -.		
CC	PIR; I51552; I51552.		
DR	HSSP; P11362; IFGK.		
DR	InterPro; IPR003599; Ig.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR011009; Kinase_like.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR001824; RecepttyrkinsIII.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	InterPro; IPR008266; Tyr_kinase_AS.		
DR	InterPro; IPR009134; VEGFR.		
DR	Pfam; PF00047; ig; 3.		
DR	Pfam; PF00069; Pkinase; 1.		
DR	PRINTS; PR01832; VEGFRECEPTOR.		
DR	ProDom; PD000001; Prot_kinase; 2.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00219; TyrKc; 1.		
DR	PROSITE; PS50835; IG LIKE; 3.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		
DR	PROSITE; PS00240; RECEPT_TYR_KIN_III; 1.		
KW	ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;		
KW	Receptor; Repeat; Signal; Transferrase; Transmembrane;		
KW	Tyrosine-protein kinase.		



```

QY 304 KVTISVHEKGFIEIKFTFSQLEAVNLHEVHFVVEVRAVPPPRISLWLNKNLTLIENLITEI 363
Db 307 KTNITVHEKGFIDLEPMFGSEEPANLHEVKSFIYNLHAYPTPGLFWLKNRNLSENLTETI 366
QY 364 TTDVEKIQIRYSKULIKLRAKEEDSGHTYIVAEQNDKAVKSYTFELLTQVPSSILDLVDD 423
Db 367 TTSIVTTKTRFOSKULIKLRAKEEDSGLYTLVAQNDKAVKSYTFELQIKVPALILSLVDK 426
QY 424 HGGSTGGQVRCVTAEGTPTLPDIEWMICKDKKCNNTSTWTLANNVSNITETIHSRDRST 483
Db 427 HGGASEQTVGLAKGMPDVEWLVCKDKRCNNDTLSILATNGSEISMETH-QDDEQ 485
QY 484 VEGRVTPAKVETPIAVCLAKNLGLAENRELKLVAPTLRSELTVAAAVLVLVIVIIISLI 543
Db 486 IESQVTFKKEIETMAIRCIATKAGNLGVVARELKLVAPTLRSELTVAAAVLVLVIVIIISLI 545
QY 544 VLVVINKQPRVIRVRVIESIPDGHGYIYVDPMLPYDSRWEFRDGLVGLRVLGSGA 603
Db 546 VLVVINKQPRVIRVRVIESIPDGHGYIYVDPMLPYDSRWEFRDGLVGLRVLGSGA 605
QY 604 FGKVGEGTAGLSRQPVVKVAVKMLKPTARSEKQALMSSELKIMTHLGHPLNIVNLLGA 663
Db 606 FGKVGEGTAGLSRQPVVKVAVKMLKPTARSEKQALMSSELKIMTHLGHPLNIVNLLGA 665
QY 664 CTKSGPIIITEYCFYGDLYNVLHKNRDSFLSHPEKPKKELDIFGLNPADESTRSYVIL 723
Db 666 CTKSGPIIITEYCFYGDLYNVLHKNRDNFQSRHPEKPKKDLDFGLNPADESTRSYVIL 725
QY 724 SPENNGDYMKGQADTQVYVPMLEKEVSKYSDIQRSLYDRPASVYKKSKMLDSEVKNLLS 783
Db 726 SPENNGDYMKGQADTQVYVPMLEKEVSKYSDIQRSLYDRPASVYKKSKPL--SEVKNLLS 783
QY 784 DNNSGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOKGIVKICDFGLARDI 843
Db 784 DGFEGELTVLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAOKGIVKICDFGLARDI 843
QY 844 MHDNSVYKSGSTFLPVKWMAPESIFDNLYTLLSDVMSYGILLWEIFSLGGTYPYGMVDS 903
Db 844 MHDNSVYKSGSTFLPVKWMAPESIFDNLYTLLSDVMSYFGLLWEIFSLGGTYPYGMVDS 903
QY 904 TFYNKIKSGYRMAKPHATSEVIEIMVKWCNSEPEKPSFYHLSELVENLLPGQYKSYTE 963
Db 904 TFYNKIKSGYRMTKPHATHEVYDIMVKWCNSEPEKPSFGLHSLDIVESLLPTEYKRCYE 963
QY 964 KTHLDFKSDHDAVARMYVDSNAYIGVTVKNEEDKLDWEGCLDQRLSADSGYIILP 1023
Db 964 TVLHDFKSDHDAVTRMRSDNSNYIGVTVKNEH-KMKDREGFDQRLSADSGYIILP 1022
QY 1024 DIDPVEEDLGRNHRSSQTSESAIETGSSSTFIKREDETIEDIMMDDIGIDSSDL 1083
Db 1023 DIDPVSDDSS-GKRNHRSSQTSESAIETGSSSTFIKREDETIEDIMMDDIGIDPSDL 1081
QY 1084 VEDSFL 1089
Db 1082 VEDSFL 1087

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## RESULT 9

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Q6P4H5 PRELIMINARY; PRT; 743 AA.
ID AC Q6P4H5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSF-
CC 1/PDGFR receptor subfamily.
DR EMBL; BC063414; AAH63414.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkiniIII.
DR InterPro; IPR002290; Ser thr pkinaase.
DR InterPro; IPR001245; Tyr pkinaase.
DR Pfam; PF00047; ig; 2.
DR PRINTS; PR01832; VEGPRECEPTOR. 1.
DR ProDom; PD0000001; Prot_kinase; 1.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
KW ATP-binding; Glycoprotein; Hypothetical protein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Transmembrane.
SQ SEQUENCE 743 AA; 82818 MW; 24564E456607649F CRC64;

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## Query Match

65.7%; Score 3715; DB 2; Length 743;

Best Local Similarity 99.9%; Pred. No. 1.7e-192;

Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCTSHPAFLVIGCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQVP 60

Db 1 MCTSHPAFLVIGCLLTGLSLILCOLSLPSILPNEKVVQLNSSFSLRCFGESEVSWQVP 60

QY 61 MSEFEESDVEIRNEENNSGLFVTVLEVSSASAAHGLTYCYVYNHTQTENELEGRIIY 120

Db 61 MSEFEESDVEIRNEENNSGLFVTVLEVSSASAAHGLTYCYVYNHTQTENELEGRIIY 120

QY 121 VPDPOVAFVPLGWTQYLVIVEDDSDSAIIPCRITTPVTLHNSGVPASVDSRQGFNG 180



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QY 61 MSEESESDVEIRNEENNSGLFVTVLEVSASAAHTGLTYCYNNHTQTEENLEGRHIYIY 120
DB 61 MSEEEDPNVEIRSEENNSGLFVTVLEVNASAAHTGMYTCYNNHTQTESEIEGRHIYIY 120
QY 121 VDDPDVAFVPLGMDTVLIVVEDDSDAIIPCRITDPTPTVTLNSEGVPASVDSRQGFNG 180
DB 121 VDDPDMAFVPLGMDTVLIVVEDDSDAIIPCRITDPTPTVTLNHNGLVFPASVDSRQGFNG 180
QY 181 TFTVGPVYICBATVKGKFKOTIPNVVALKATSELDLEMEALKTIVYKSGETIVVTVCAVFN 240
DB 181 TFSVGPIYICBATVKGKFKOTIPNVVALKATSELDLEMEALKTIVYKSGETIVVTVCAVFN 240
QY 241 EYVDLQWTFYGEVKGKGIITLMEIEIKVPSIKLVYTLVTPVATVKSQDGYECAARQATREVK 300
DB 241 EYVDLQWTFYGEVKGKGIITLMEIEIKVPSIKLVYTLVTPVATVKSQDGYECAARQATREVK 300
QY 301 EMKVTISVHEKGFIBIKPTFSQLEAVNLHVKHFVVEVRAYPPPRISWLNKNTLIENL 360
DB 301 EMKVRTISVHEKGFIBIKPTFSQLEAVNLHVKHFVVEVRAYPPPRISWLNKNTLIENL 360
QY 361 TEITDVEKIOETRYVSKLIRAKEDSGHYTIVAQNEADAVKSYTFELLTQVPSILD 420
DB 361 TEITDVEKIOETRYVSKLIRAKEDSGHYTIVAQNEADAVKSYTFELLTQVPSILD 420
QY 421 VDDHSGTGGQVRCVTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNITTEIHSRD 480
DB 421 VDDHSGTGGQVRCVTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNITTEIHSRD 480
QY 481 RSTVEGRVTFPAKVEETIAVCLAKNLLGAENRELKLVAPTLSRELVAVALVLLVIV 540
DB 481 RSTVEGRVTFPAKVEETIAVCLAKNLLGAENRELKLVAPTLSRELVAVALVLLVIV 540
QY 541 SLIVLVVWKQPRYEIRVRVIESISPDGHEYIYVDPMLPYDSRWEFPRDGLVLRVLG 600
DB 541 SLIVLVVWKQPRYEIRVRVIESISPDGHEYIYVDPMLPYDSRWEFPRDGLVLRVLG 600
QY 601 SGAFGKVBEGTAYGLSRSPVMKVAVKMLKPTARSEKQALMSKIMTHLGLPHLNVNL 660
DB 601 SGAFGKVBEGTAYGLSRSPVMKVAVKMLKPTARSEKQALMSKIMTHLGLPHLNVNL 660
QY 661 LGACTSGPIIYITEYCFYGDVLYNHLKNDSPSHHPKPKKELDI FGLNPADESTRSY 720
DB 661 LGACTSGPIIYITEYCFYGDVLYNHLKNDSPSHHPKPKKELDI FGLNPADESTRSY 720
QY 721 VILSPENNGDYMCKQADTTQVVPMLERKEVSKYDIQRLSYDRPASYYKKSM 774
DB 721 VILSPENNGDYMCKQADTTQVVPMLERKEVSKYDIQRLSYDRPASYYKKSM 774
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RESULT 11  
Q8AXC7 PRELIMINARY; PRT; 1062 AA.  
AC Q8AXC7;  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Takifugu.  
OC NCBI\_Taxid=31033;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22481137; PubMed=12592706;  
RA Williams H., Brenner S., Venkatesh B.;  
RT "Characterization of the platelet-derived growth factor receptor alpha  
and c-kit genes in the pufferfish Fugu rubripes.";  
RL DNA Seq. 13:263-270(2002).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSP-1/PDGF receptor subfamily.  
CC EMBL; AF456419; AAN87554.1; -;  
DR HSSP; P36888; 1RJB.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0005524; F: ATP binding; IEA.  
DR GO; GO:0004872; F: receptor activity; IEA.  
DR GO; GO:0016740; F: transferase activity; IEA.  
DR GO; GO:0005021; F: vascular endothelial growth factor receptor; IEA.  
DR GO; GO:000468; P: protein amino acid phosphorylation; IEA.  
DR GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. .; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR001824; RecepttyrkinsIII.  
DR InterPro; IPR001245; Tyr\_kinase\_AS.  
DR InterPro; IPR008286; Tyr\_kinase\_AS.  
DR Pfam; PF00047; IG; 1.  
DR PRINTS; PR01832; VEGFRECEPTOR.  
DR ProDom; PD000001; Prot\_kinase; 2.  
DR SMART; SM00409; IG; 3.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00109; PROTEIN KINASE\_TYR; 1.  
DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;  
KW Phosphorylation; Receptor; Transferase; Transmembrane;  
KW Tyrosine-protein kinase.  
SQ SEQUENCE 1062 AA; 118636 MW; 5439854FE1748832 CRC64;

Query Match 60.5%; Score 3419.5; DB 2; Length 1062;  
Best Local Similarity 62.5%; Pred. No. 2.7e-176;  
Matches 668; Conservative 145; Mismatches 240; Indels 15; Gaps 8;

QY 26 SLPSILPNEKVKVQLNSSFRCFGESEVSWQYPMSEBESSDVEIRNEENNSGLFVTVL 85  
DB 6 SAPLLLPQLEELVPLVHTAFTLTCCGEATINDVPL-----DVPEKTQEDNSGLFVTVI 59  
QY 86 EYSSASAAHTGLTYCYNNHTQTEENLEGRHIYIYVDPDPAFVPLGMDTVLIVVEDDSD 145  
DB 60 SVDSASAMHTGYVRCFYRRNATEDADEAMQSIYVYVDPDPAFVPLVFPNGHVLSDHEE 119  
QY 146 AIIPCRTDPTPTVTLN--SEGVPASVDSRQGFNGTETVGPYICBATVKGKFKOTIP 203  
DB 120 MEIQCRVSPSANVTLLINVDITQOPVPCMYDSKRGALGVFTAGTYVCKGVNGAEHYS 179  
QY 204 NVVALKATSELDLEMEALKTIVYKSGETIVVTVCAVFNNEVVDLQWTFYGEVKGKGIITL 263  
DB 180 IVHGWIGGSGLVHVELTAKHTVLLVGDITVNCCLAQSEILEDHMKYPGKVANRAIKTVH 239  
QY 264 IKVPSIKLVYTLVTPVATVKSQDGYECAARQATREVKEMKKTIVSVHEKGFIBIKPTFSQ 323  
DB 240 NKDKQ-EILYTLTVPOASVKDGIYSCSITDVVNNSTQKQIAIRVAVSEFMSIQPKFGE 298  
QY 324 LEAVNLHVKHFVVEVRAYPPPRISWLNKNTLIENLTITDVEKIOETRYVSKLIR 383  
DB 299 YFSAELDEYCEFAEITSPFTASVTWFKDSVPLSNVTABISTLSQKLSETSYMSVLTLIR 358  
QY 384 AKEEDSGHYTIVAQNEADAVKSYTFELLTQVPSILDVDDHSGTGGQVRCVTAEGTPLP 443  
DB 359 AKEEDSGNTVMRVKGDQSRVLSLILEVKVPAVIVDLMDIHGSAVGQSVVCLITRQPTP 418  
QY 444 DIEWMICKDIKKCNNET-SWTILANNVSNITTEIHSRDRSTVEGRVTFPAKVEETIAVRCL 502  
DB 419 LVWEFVCKNIKHCANDTSSWVPLPVNSTEVTWDSRFDENNLLETQVIFGHELENTLAVRCL 478  
QY 503 AKNLLGAENRELKLVAPTLSRELVAVALVLLVIVISLIVLVVWKQPRYEIRVRV 562  
DB 479 ARNEMAAVSRKIKLVNSGPHPELTVAVALVLLVIVISLIVLVVWKQPRYEIRVRV 538



QY 563 ESISPDGHEIYVDPMQLPYDSRWEPRDGLVLRVLGSGAGKVVGGTAYGLSRSQPW 622  
 DB 539 ESUSPDGHEIYVDPMQLPYDSRWEPRDRLVLRVLGSGAGKVVGGTAYGLSRSQPW 598  
 QY 623 KVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNLGACTKSGPIIITEYCFYGL 682  
 DB 599 KVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNLGACTKSGPIIITEYCFYGL 658  
 QY 683 VNYLHKRDSPLSHHEKP-KKELDIFGLNPADESTRSVIISFENNGDYMMDKQADTTQ 741  
 DB 659 VNYLHKRDSFLNPKPKKELDIFGINPADESSRYVILSFESKGDYMDKQADNTQ 718  
 QY 742 YVPMLEKEVSKYSDIORSLYDRPASVYKSKMLSDVSKMLSDNSSEGLTLLDLSFTYQ 801  
 DB 719 YVPMLEISNAKYSVDLQGNHYDPPSKGNS--DGMQDQLSDNMSGLTLLDLSFTYQ 776  
 QY 802 VARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLARDIMHDSNVYKSGSTFLPVKW 861  
 DB 777 VARGMEFLASKNCVHRDLAARNVLLSQKIVKICDFGLARDIMHDSNVYKSGSTFLPVKW 836  
 QY 862 MAPESIFDNLTYTLDVWSYGILLWEIFSLGTPYPCMAVDSTFYNKIKSGYRMAKPDHA 921  
 DB 837 MAPESIFDNLTYTLDVWSYGILLWEIFSLGTPYPCMAVDSTFYNKIKSGYRMAKPDHA 896  
 QY 922 TSEVYIMVKWNSPEKPSFVHLSEIIVENLLPGQYKSKYKIHLDLFLKSDHPAVARWR 981  
 DB 897 PQDVYDMKWCNSPEKPSFVHLSEIIVENLLPGQYKSKYKIHLDLFLKSDHPAVARWR 956  
 QY 982 VPSDNIAYIGVYKNEEDKLKDWEGGLDEORLSADSGYIIPLDIPDPVPEEDLKGKRNHS 1041  
 DB 957 VDNDDAYIGITKN-QGKLDRESGDEORLSADSGYIIPLDIPDPISDEE-YGKRNHS 1014  
 QY 1042 SQTSESATETGSSSTTFKREDETIEDIMDDIDIGSDLDVDSFL 1089  
 DB 1015 SQTSESATETGSSSTTFKREDETIEDITLDEMCLDCLDVDSFL 1062

RESULT 12  
 Q9DE49 PRELIMINARY; PRT; 1059 AA.  
 AC Q9DE49  
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Platelet-derived growth factor receptor alpha.  
 GN Names=pgdfr;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Liu L., Balasubramanian N.V., Ge R.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSP-1/PDGF receptor subfamily.  
 DR EMBL; AF200951; AAG43479.1; -;  
 DR HSP; P36888; 1RJB.  
 DR ZFIN; ZDB-GENE-990415-208; pgdfr.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR001824; RecepttyrklnsIII.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008266; Tyr\_kinase\_AS.  
 DR InterPro; IPR009134; VEGFR.  
 DR Pfam; PF00047; Ig; 1.  
 DR PRINTS; PRO1832; VEGPRECEPTOR.  
 DR ProDom; PD000001; Prot\_kinase; 2.  
 DR SMART; SM00408; Igc2; 1.  
 DR SMART; SM00219; Tyrcg; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
 KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;  
 KW Phosphorylation; Receptor; Transferase; Transmembrane;  
 KW Tyrosine-protein kinase.  
 SQ SEQUENCE 1059 AA; 118210 MW; 0AE93E2ABD9A72F3 CRC64;  
 Query Match 59.5%; Score 3363; DB 2; Length 1059;  
 Best Local Similarity 61.5%; Pred. No. 3e-173;  
 Matches 659; Conservative 157; Mismatches 223; Indels 32; Gaps 14;  
 QY 28 PSILPNEKVVQLNSSFSLRCFSGSEVSWQYPM-SEESSDVEIRNEENNGLFVTVLE 86  
 DB 12 PLIWPQRESMEVSLHSTFLRCGTQELSWNGFVTDQTSVK-----KGLFISTVT 64  
 QY 87 VSSASAAHGLTCY---YNHQTQTEENLEGRHVIYVDPDVAFVPLGMDTY-LIVED 142  
 DB 65 ISNATAVTHGEVCSSEPFNSTEST-----IYIVDPDQTPFPV-SMTFENHVLTS 115  
 QY 143 DSAIIPCTRTDPEPTVTL--HNSGVVPASYSRQGFNGTFTVGPYICEATVKGKKFOT 200  
 DB 116 YDEMEIPCHVTDPASVSLIHMGTVQVMSAYDSKRGFGLGAGTYVCRALIHQNHDS 175  
 QY 201 IPNVVALKATSELDLEMEALTKVYKSGETIVVTCVAFNNEVDLOWTPGVEKKGITM 260  
 DB 176 IEYIVHGVTGGSDLRVELRAVRKRTLLVGETITVDCVAKGSEVLEDHWKYPGLANRGPKT 235  
 QY 261 LEEIKVPSIKLVYTLTVPKATVDCGYECAAQATREVKEMKVKVTISVHEKGFIEIKPT 320  
 DB 236 VRENKL-NLEIYITVTVTNAPSDSGIYACSTIDMSNESQTKELTITVDFHVFHINFL 294  
 QY 321 FSQLEAVNLHVKHFVVEVRAYPPIPRISWLNKNTLIENLTITTDVEKIQEIRYSKIK 380  
 DB 295 IGPVETARLDEVPFVKVDIESFPAPKVTWLKSSVLGDDTAETISTLLKIGETSYQGVLN 354  
 QY 381 LIRAKEEDSGHTYVAONEDAVKSYTFELLTOVPSILDLVDHSGSTGGTVRCATGTT 440  
 DB 355 LIRAKAEDSGNTYKAEIGSISTSYFLQVPPVIVDLIDVHGSAAAGQEVVCTAGGS 414  
 QY 441 PLPDIEMWICKDKKCNNTS-WTILANNVSNITIEHSRDRSTVEGRVTFKVEETIAV 499  
 DB 415 PPEVDWDICKNLKCKANDSQWMLPINSTDITVELQNVNDNHIESHIFHLEGTAV 474  
 QY 500 RCLAKNLLGAENRELKVAPTLRSELTAAAVLVLLVIVIIISLIVLVWIKQKPRYEIRW 559  
 DB 475 RCLARNDMGVSVREVKLMSGPHSELTVAAAVLVLLVIVIIISLIVLVWIKQKPRYEIRW 534  
 QY 560 RVIESISPDGHEIYVDPMQLPYDSRWEPRDGLVLRVLGSGAGKVVGGTAYGLSRSQ 619  
 DB 535 RVIESISPDGHEIYVDPMQLPYDSRWEPRDGLVLRVLGSGAGKVVGGTAYGLSRSQ 594  
 QY 620 PVMKAVAKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNLGACTKSGPIIITEYCFY 679  
 DB 595 PVMKAVAKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNLGACTKSGPIIITEYCFY 654  
 QY 680 GDLVNYLHKRDSFLSHHEKPKKELDIFGLNPADESTRSVIISFENNGDYMMDKQADT 739  
 DB 655 GDLVNYLHKRDSFLSRHTEKGGKLDIFGINPADESSRYVILSFESKGDYMDKQADT 714  
 QY 740 TQVPMLEKEVSKYSDIORSLYDRPASVYKSKMLSDVSKMLSDNSSEGLTLLDLSFT 799



Db 715 MQVPMLENNASKYPIQRSDYDHPSPHRQ---FNDEAESLLSDPSAEGLTMDLLSFT 771

QY 800 YQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLARDIMHDSNTVSKGSTFLPV 859

Db 772 YQVARGMEFLASKNCVHRDLAARNVLLSQKIVKICDFGLARDIMHDSNTVSKGSTFLPV 831

QY 860 KMWAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTYPGMMVDSTFYNKIKSGYRMKAPD 919

Db 832 KMWAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTYPGMMVDSTFYNKIKSGYRMKAPD 891

QY 920 HATSEVVEIMVKNWSEPEKPSFYHLSEIVENLLPGQYKSKYEKTHLDFLKSDEHFAVAR 979

Db 892 HASSDYELMMKWCNSEPEKPSFHLSDTVALSPSGFKRCYRVNWHDFLKSDEHFAVAR 951

QY 980 MR-VDSNDYAYIGVYKNEEDKLDWGGGLDEQRLSDSGYIIPLPIDPVPPEEDLGKRN 1038

Db 952 VQCIDNDYAYGVLYKN-QCKMKTRESGDEQRLSDSGYIIPLPIDLP-SNEDYSKRN 1009

QY 1039 RHSSQTSSESAITGSSSTFFIKREDTIEDIDMDIDGIDSDLVEDSFL 1089

Db 1010 RHSSQTSSESAITGSSST-TKREGTLEDITLLDEMCLDSDGLVEDSFL 1059

RESULT 13

Q8AXC8 PRELIMINARY; PRT; 1078 AA.

AC Q8AXC8

DT 01-MAR-2003 (Tr-EMBLrel. 23, Created)

DT 01-MAR-2003 (Tr-EMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (Tr-EMBLrel. 26, Last annotation update)

DE PDGFRalpha isoform 2.

GN Names:PDGFRalpha;

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Takifugu.

OX NCBI\_TaxID=31033;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22481137; PubMed=12592706;

RA Williams H., Brenner S., Venkatesh B.;

RT "Characterization of the platelet-derived growth factor receptor alpha

RT and c-kit genes in the pufferfish Fugu rubripes.";

RL DNA Seq. 13:263-270(2002).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. CSP-

CC 1/PDGFR receptor subfamily.

DR EMBL; AF456419; AAN87556.1; -.

DR HSSP; P36888; 1RJB.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:005524; F:ATP binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.

DR InterPro; IPR0031599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR011009; Kinase\_like.

DR InterPro; IPR0070719; Prot\_kinase.

DR InterPro; IPR001824; RecepttyrkinsII.

DR InterPro; IPR001245; Tyr\_pkinase.

DR InterPro; IPR008266; Tyr\_pkinase\_AS.

DR InterPro; IPR009134; VEGFR.

DR Pfam; PF00047; ig; 1.

DR PRINTS; PR01832; VEGFRRECEPTOR.

DR ProDom; PD000001; Prot\_kinase; 2.

DR SMART; SM00409; IG; 3.

DR SMART; SM00219; Tyrc; 1.

DR PROSITE; PS50835; IG\_LIKE; 2.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.

KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;

KW Phosphorylation; Receptor; Transferase; Transmembrane;

KW Tyrosine-protein kinase.

SQ SEQUENCE 1078 AA; 120388 MW; 458576D8D190BD0 CRC64;

Query Match 58.3%; Score 3296; DB 2; Length 1078;

Best Local Similarity 60.2%; Pred. No. 1.3e-169;

Matches 662; Conservative 148; Mismatches 245; Indels 44; Gaps 16;

QY 8 FLVLGCLLGLSLILCOLSLPSILPNENKVKVQNLNSFSRLRCGESEVSHQYPMSEESS 67

Db 7 YVVFVGIL--VWSVTSLSPPTIVSNEEEFILLPSSILANVSCVCKRNVVMAEPL----- 58

QY 68 DVEIRNEKNS---GLFVTLVSVSSAAHTGLTYCYNHTQTEE-----NELGRH 116

Db 59 -----PNSFVFPQYTTATLFYNATVNTVNTYTTCTVYVHLAEQGGQOEANEAB--- 108

QY 117 IYIVVDPDPVAFVPLGMDYLVIVEDDSALIPRTTDPETVTLHN--SEG-VVPASYS 174

Db 109 IYVVFDAQVPFVP-ETPDNLVVTMDPSGVPISCRVSDDPHSHVTLRSVSTGDEMSAFYDG 167

QY 175 RQGFNGTFTVGPYICEATVKGKFKQIPFNVAL--KATSELDLEMEALKTIVYKSGETIV 232

Db 168 RIGFFGLSPGQYQCETFFVNGRIFRS---DIYVDEGGSGGLHVELTAKHTVLLVAGDTIT 224

QY 233 VTCAVENNEVDLQWTPGSEVKGKGTMLLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292

Db 225 VNCLAGSEILDEHWKYPQKVNRAIKVHENKKQ-QEILYTLTVPQASVKDGIYVCS 283

QY 293 RQATREVEMKMKVTISVHEKGFTEIKPTFSQLEAVNLHEVKEFVVEVYRPPRISWLKN 352

Db 284 TDVVTNMSQTKQIAIRVASEFMSIQPKGEYESSAELDEVCEFAEITSPPTASVTWFKD 343

QY 353 NLTLIENLTETITDVEKIQEIRYRSKLIKIRAKEEDSGHYTIVAQEDAVKSTFELLTQ 412

Db 344 SVPLSNVTAEISTLSQKSETSYMSVLTITLIRAKEEDSGNVTMRVKGNGDQSRVTSILLEV 403

QY 413 VPSSILDLVDHGGTGGOTVRCATRGTPLPDTEWMIKCKDIKKONNET-SWTLANNVSN 471

Db 404 VFVAVLDLMDIHHGSATGQSVVCITRGQPTPLVFWFCVKNIKHCAKNDTSWVPLPVNSTE 463

QY 472 IITEHSRDRSTVEGRVTFKAVETIATVACLAKNLGAENRELKLVAPTLRSELTVAAAV 531

Db 464 VTMDSRFEDNNLEQTQVIFGHLENTLAVRCLARNEMAASREIKLVSGNPHPELTVA 523

QY 532 LVLLVIVIIISLVVVIWQKPRYETRWVIESISPDGHEIYIVDPMQLPYDSRWEPPRD 591

Db 524 LVLLVIVIIISLVVVIWQKPRYETRWVIESVSPDGHEIYIVDPMQLPYDSRWEPPRD 583

QY 592 GLVIGRVLGSGAGKVEGTAYGLSRSPQPMKVAVKMLKPTARSSKQALMSLKTMTLH 651

Db 584 RLVLGRLGSGAGKVEGTAYGLSRSPQPMKVAVKMLKPTARSSKQALMSLKTMTLH 643

QY 652 GPHLNIIVNLGACTSGPIIITEYCFYGDVNLVHLKRDSTFLSHPEKP-KKELDIFGL 710

Db 644 GPHLNIIVNLGACTSGPIIITEYCFYGDVNLVHLKRDSTFLSHPEKP-KKELDIFGI 703

QY 711 NPADESTRSYVILSPENNGDYMDKQADTTQVYVPMLEKVEKSYSDIQRSLYDRPASYKK 770

Db 704 NPADESTRSYVILSPESKGDYMDKQADNTQVYVPMLEISNASKYSDLQGSNYOHPHSQK 763

QY 771 KSMLDSEVNKLSDDNSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQK 830

Db 764 SN--DGMQLDSDNMSEGLTNDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQQK 821

QY 831 IVKICDFGLARDIMHDSNTVSKGSTFLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFS 890

Db 822 IVKICDFGLARDIMHDSNTVSKGSTFLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFS 881

QY 891 LGGTPYGMVVDSTFFYNKIKSGYRMKAPDHATSEVTEIMVKWCNSEPEKPSFYHLSEIV 950

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Db 882 LGCTPYGMIIVDSFYNKIKSGYRMSKPEHAPQDVYDMVMKWCNSPEKRPSPFLGLSDTI 941
QY 951 ENLLPQYKKSYEKIHLDFKSDHPAVARMRVDSNAYIGVTYKNEEDKLKOWEGLDEQ 1010
Db 942 ASLLPSYKRHYRVNHEFLKSDHPAVTRVCVNDNDAYIGITYKN-OGKLRKORESGFDEQ 1000
QY 1011 RLSADSGYIIPLDIPDPVEEEDLGRNRHSSQTSESAIETGSSSTFIKREDETIEDI 1070
Db 1001 RLSADSGYIIPLDIPDPVEEEDLGRNRHSSQTSESAIETGSSSTFIKREDETIEDI 1059
QY 1071 DMDDIGIDSDLVDSFL 1089
Db 1060 TLLDEMCLDCSLVDSFL 1078

RESULT 14
ID Q72608 PRELIMINARY; PRT; 849 AA.
AC Q72608;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FIP1LI/PDGFR fusion protein.
GN Name=FIP1LI/PDGFR fusion protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12808148; DOI=10.1073/pnas.0932698100;
RA Griffin J.H., Leung J., Bruner R.J., Calliguri M.A., Briesewitz R.;
RT "Discovery of a fusion kinase in EOL-1 cells and idiopathic
RT hyperosinophilic syndrome."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7830-7835(2003).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. CSP-
CC 1/PDGFR receptor subfamily.
DR EMBL; AY228992; AAP69563.1; -.
DR HSSP; P36888; IRJB.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IEA.
DR InterPro; IPR007854; Fip1.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_Pkinase_AS.
DR Pfam; PF05182; Fip1; 1.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 849 AA; 94703 MW; 597527ED06A129FF CRC64;

Query Match 47.6%; Score 2692; DB 2; Length 849;
Best Local Similarity 74.6%; Pred. No. 4.3e-137;
Matches 551; Conservative 28; Mismatches 61; Indels 99; Gaps 12;

QY 352 NMLTLENLTETITDVEKQIEYRSLKILIRAKEDSGHYTIVAQNEADAVKSYTFELLT 411
Db 209 NKITAEDCTMEVTPGAE-IQDGRF-----NLFKVOQGRGTGN-----SEKETALPSTKAE-FT 558

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QY 412 QVPSSILDLVDHGGSTGGQTVRCATGTPLPDIEWMKICKIKCNNET-SWTLANNVS 470
Db 259 SPSPFKTGLPSPRNSTSSQSTSTAS-----RKANSVGVKW----- 295
QY 471 NIITEIHSRDRSTVEGRVTFKAVEETIAVRCLAKNLGAENRELKLVAPTLRSELVAAA 530
Db 296 -----QDR-----YGRAE-----SPDLR-----RLPGA 313
QY 531 VLVLVIVIVISLVLVWVKQPRYEIRWRVIESISPDGHEIYYVDPMPOLPYDSRWEFFR 590
Db 314 IDVIGQITITIS-----RVEGRRRANNSN-----IQLPYDSRWEFFR 350
QY 591 DGLVLRVLGSGAFKGVVEGTAYGLSRSQPVKMKAVKMLKPTARSEKQALMSELKIMTH 650
Db 351 DGLVLRVLGSGAFKGVVEGTAYGLSRSQPVKMKAVKMLKPTARSEKQALMSELKIMTH 410
QY 651 LGPHLNVNLLGACTKSGPIIYIITEYCFYGDVLVNYLHKRDSFLSHHPKPKKELDIFGL 710
Db 411 LGPHLNVNLLGACTKSGPIIYIITEYCFYGDVLVNYLHKRDSFLSHHPKPKKELDIFGL 470
QY 711 NPADESTRSYVILSPENNGDYMDKQADTTQVYVPMLEKEVSKYSDIQSLYDRPASYKK 770
Db 471 NPADESTRSYVILSPENNGDYMDKQADTTQVYVPMLEKEVSKYSDIQSLYDRPASYKK 530
QY 771 KSMLESEVKNLLSDDNSEGLTLILLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQQK 830
Db 531 KSMLESEVKNLLSDDNSEGLTLILLSTFYQVARGMEFLASKNCVHRDLAARNVLLAQQK 590
QY 831 IVKICDFGLARDIMHDSNVSKGSTPLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFS 890
Db 591 IVKICDFGLARDIMHDSNVSKGSTPLPVKMWAPESIFDNLYTTLSDVMSYGILLWEIFS 650
QY 891 LGCTPYGMIIVDSFYNKIKSGYRMAKPDHATSEVVEIMVKWCNSPEKRPSPFHLSEIV 950
Db 651 LGCTPYGMIIVDSFYNKIKSGYRMAKPDHATSEVVEIMVKWCNSPEKRPSPFHLSEIV 710
QY 951 ENLLPQYKKSYEKIHLDFKSDHPAVARMRVDSNAYIGVTYKNEEDKLKOWEGLDEQ 1010
Db 711 ENLLPQYKKSYEKIHLDFKSDHPAVARMRVDSNAYIGVTYKNEEDKLKOWEGLDEQ 770
QY 1011 RLSADSGYIIPLDIPDPVEEEDLGRNRHSSQTSESAIETGSSSTFIKREDETIEDI 1070
Db 771 RLSADSGYIIPLDIPDPVEEEDLGRNRHSSQTSESAIETGSSSTFIKREDETIEDI 830
QY 1071 DMDDIGIDSDLVDSFL 1089
Db 831 DMDDIGIDSDLVDSFL 849

RESULT 15
PGDR HUMAN
ID PGDR_HUMAN STANDARD; PRT; 1106 AA.
AC P09619; Q8N5L4;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Beta platelet-derived growth factor receptor precursor (EC 2.7.1.112)
DE (PDGF-R-beta) (CD140b antigen).
GN Name=PDGFRB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88217915; PubMed=2835772;
RA Gronwald R.G.K., Grant F.J., Haldeman B.A., Hart C.E., O'Hara P.J.,
RA Hagen F.S., Ross R., Bowen-Pope D.F., Murray M.J.;
RT "Cloning and expression of a cDNA coding for the human platelet-
RT derived growth factor receptor: evidence for more than one receptor
RT class."
RN Proc. Natl. Acad. Sci. U.S.A. 85:3435-3439(1988).
RN [2]

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RP SEQUENCE FROM N.A.  
 RX MEDLINE=89096941; PubMed=2850496;  
 RA Claesson-Welsh L., Eriksson A., Moren A., Severinsson L., Ek B.,  
 RA Oestman A., Betsholtz C., Heldin C.-H.;  
 RT "cDNA cloning and expression of a human platelet-derived growth factor  
 RT (PDGF) receptor specific for B-chain-containing PDGF molecules.";  
 RL Mol. Cell. Biol. 8:3476-3486 (1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Musny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RP SEQUENCE OF 548-569 FROM N.A.  
 RX MEDLINE=97429921; PubMed=9285559; DOI=10.1038/sj.onc.1201267;  
 RA Chi K.D., McPhee R.A., Wagner A.S., Dietz J.J., Pantazis P.,  
 RA Goustin A.S.;  
 RT "Integration of proviral DNA into the PDGF beta-receptor gene in HTLV-  
 RT I-infected T-cells results in a novel tyrosine kinase product with  
 RT transforming activity.";  
 RL Oncogene 15:1051-1057 (1997).  
 RN [5]  
 RP SEQUENCE OF 1046-1106 FROM N.A.  
 RX MEDLINE=89028677; PubMed=2846185; DOI=10.1016/0092-8674(88)90224-3;  
 RA Roberts W.M., Look A.T., Roussel M.F., Sherr C.J.;  
 RT "Genetic linkage of human CSF-1 receptor (c-fms) and PDGF receptor  
 RT tandem.";  
 RL Cell 55:655-661 (1988).  
 RN [6]  
 RP SEQUENCE OF 33-47.  
 RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites.";  
 RL Protein Sci. 13:2819-2824 (2004).  
 RN [7]  
 RP AUTOPHOSPHORYLATION SITES.  
 RX MEDLINE=89376563; PubMed=2550144; DOI=10.1016/0092-8674(89)90510-2;  
 RA Kazlauskas A., Cooper J.A.;  
 RT "Autophosphorylation of the PDGF receptor in the kinase insert region  
 RT regulates interactions with cell proteins.";  
 RL Cell 58:1121-1133 (1989).  
 RN [8]  
 RP INTERACTION WITH APS.  
 RX MEDLINE=99142932; PubMed=9989826; DOI=10.1038/sj.onc.1202326;  
 RA Yokouchi M., Wakioka T., Sakamoto H., Yasukawa H., Ohtsuka S.,  
 RA Sasaki A., Ohtsubo M., Vallius M., Inoue A., Komiya S., Yoshimura A.;  
 RT "APS, an adaptor protein containing PH and SH2 domains, is associated  
 RT with the PDGF receptor and c-Cbl and inhibits PDGF-induced  
 RT mitogenesis.";  
 RL Oncogene 18:759-767 (1999).  
 RN [9]  
 RP CHROMOSOMAL TRANSLOCATION WITH TRIP11.  
 RX MEDLINE=98043615; PubMed=9373237;

RA Abe A., Emi N., Tanimoto M., Terasaki H., Marunouchi T., Saito H.;  
 RT "Fusion of the platelet-derived growth factor receptor beta to a novel  
 RT gene CEV14 in acute myelogenous leukemia after clonal evolution.";  
 RL Blood 90:4271-4277 (1997).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.79 ANGSTROMS) OF 751-755 IN COMPLEX WITH  
 RP PIK3R1, AND COMPARISON WITH NMR ANALYSIS.  
 RX MEDLINE=21450159; PubMed=11567151; DOI=10.1107/S0907444901012434;  
 RA Fauptit R.A., Dennis C.A., Derbyshire D.J., Breeze A.L., Weston S.A.,  
 RA Rowsell S., Murshudov G.N.;  
 RT "NMR trial models: experiences with the colicin immunity protein Im7  
 RT and the p8SalpHa C-terminal SH2-peptide complex.";  
 RL Acta Crystallogr. D 57:1397-1404 (2001).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1102-1106 IN COMPLEX WITH  
 RP SLC9A3R1 AND PDGFRA.  
 RX MEDLINE=22013966; PubMed=11882663; DOI=10.1074/jbc.M201507200;  
 RA Karthikeyan S., Leung T., Ladias J.A.A.;  
 RT "Structural determinants of the Na+/H+ exchanger regulatory factor  
 RT interaction with the beta 2 adrenergic and platelet-derived growth  
 RT factor receptors.";  
 RL J. Biol. Chem. 277:18973-18978 (2002).  
 CC -!- FUNCTION: Receptor that binds specifically to PDGFB and has a  
 CC tyrosine-protein kinase activity. Phosphorylates Tyr residues at  
 CC the C-terminus of PTPN11 creating a binding site for the SH2  
 CC domain of GRB2.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBUNIT: Homodimer, and heterodimer with PDGFRA. Interacts with  
 CC APS.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- DISEASE: Involved in a form of chronic myelomonocytic leukemia  
 CC (CMML) characterized by abnormal clonal myeloid proliferation and  
 CC by progression to acute myelogenous leukemia (AML) through a  
 CC chromosomal translocation t(5;12)(q33;p13) that involves PDGFRB  
 CC and ETV6/TEL.  
 CC -!- DISEASE: Involved in a acute myelogenous leukemia through a  
 CC chromosomal translocation t(5;14)(q33;q32) that involves PDGFRB  
 CC and TRIP11. The fusion protein may be involved in clonal evolution  
 CC of leukemia and eosinophilia.  
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF  
 CC receptor subfamily.  
 CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.  
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 CC -----  
 CC EMBL; J03278; AAA60049.1; -.  
 CC EMBL; M21616; AAA36427.1; -.  
 CC EMBL; U33172; AAC51675.1; -.  
 CC EMBL; BC032224; AAA32224.1; -.  
 CC PIR; A28206; PFHUGB.  
 CC PDB; 1G05; X-ray; A=1102-1106.  
 CC PDB; 1H90; X-ray; B=751-755.  
 CC PDB; 1LWP; Model; A=600-962.  
 CC Genew; HGNC:8804; PDGFRB.  
 CC H-InvDB; HIX0005310; -.  
 CC MIM; 173410; -.  
 CC GO; GO:0004992; F:platelet activating factor receptor activity; TAS.  
 CC GO; GO:0005017; P:platelet-derived growth factor receptor act. . . ; TAS.  
 CC GO; GO:0007165; P:signal transduction; TAS.  
 CC InterPro; IPR007110; IG-like.  
 CC InterPro; IPR003598; IG\_c2.  
 CC InterPro; IPR011009; Kinase like.  
 CC InterPro; IPR000719; Prot\_kinase.  
 CC InterPro; IPR001824; RecepttyrkinIII.  
 CC InterPro; IPR001245; Tyr\_pkinase.  
 CC InterPro; IPR008266; Tyr\_pkinase\_AS.

